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Page, Thurman

Sent:

Friday, June 18, 2004 2:31 PM

To:

STIC-Biotech/ChemLib

Cc:

Basi, Nirmal; Page, Thurman

Subject:

FW: Rush sequence esrch for App No. 09/429,832 (use squence listing in parent

08/906,365case to do the search)

TWO MONTH AMENDMENT: RUSH SEARCH APPROVED

Thurman K. Page SPE Art Units 1615 & 1616 **Technology Center 1600**

----Original Message----From:

Basi, Nirmal

Sent:

Friday, June 18, 2004 1:21 PM

To:

Page, Thurman

Subject:

FW: Rush sequence esrch for App No. 09/429,832 (use squence listing in parent 08/906,365case to do the search)

Thurman, Cristina is out of the office, could you approve a rush search please.

----Original Message----

From:

Basi, Nirmal

Sent:

Friday, June 18, 2004 1:18 PM

To:

Chan, Christina

Subject:

Rush sequence esrch for App No. 09/429,832 (use squence listing in parent 08/906,365case to do the search)

Christina I am seeking approval for a RUSH sequence search, as indicated below. If approved, could you please forward the search to STIC and cc a copy to me.

Examiner: Nirmal S. Basi

Art Unit 1646

Office: Remsen Building, Room 4D68 Mail Room: Remsen Building, room 4C70

Sequence search:

App. #: 09/429,832 (please use the sequence listing in parent application 08/906,365 to do the search)

Result format: Paper.

Title NOVEL HUMAN ESTROGEN RECEPTOR-BETA

Inventors: BHAT, RAMESH A. et al

Priority Date: 8/5/97

Please search: SEQ ID NO:2

Searcher:	an
Phone:	172504
Location:	<u> </u>
Date Picked Up:	6120
Date Completed:	6/20
Searcher Prep/Rev	iew:
Clerical:	
Online time:	<i>(1</i>)

TYPE OF SEARCH:	
NA Sequences:	
AA Sequences:	_
Structures:	_
Bibliographic:	
Litigation:	
Full text:	_
Patent Family:	
Other	

/ENDOR/COST (w	here applic.)
STN:	
DIALOG:	
Questel/Orbit:	
DRLink:	
Lexis/Nexis:	
Sequence Sys.:	,
WWW/Internet:_	
Other (specify):	

Search commercial, issued and interference databases.

Thanks, Nirmal S. Basi

$\langle \cdot \rangle \langle \cdot \rangle \sim$
Searcher:
Phone: 12504
Location:
Date Picked Up: 10 20
Date Completed: 6/20
Searcher Prep/Review:
Clerical:
Online time:
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TYPE OF SEARCH:	
NA Sequences:	
AA Sequences:	
Structures:	
Bibliographic:	
Litigation:	
Full text:	
Patent Family:	
Other:	

VENDOR/COST (where app	lic.)
STN:	
DIALOG:	
Questel/Orbit:	
DRLink:	
Lexis/Nexis:	
Sequence Sys.:	
WWW/Internet:	
Other (specify):	

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Sequence 2, Appli
Sequence 106, App
Sequence 3, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 13, Appli
Sequence 14, Appl
Sequence 14, Appl
Sequence 15, Appli
Sequence 5, Appli
Sequence 2, Appli
                                                                                                June 20, 2004, 10:38:43; Search time 49 Seconds (without alignments) 3053.597 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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2805
1 MDIKNSPSSINSPSSYNCSQ......ECSPAEDSKSKEGSQNPQSQ
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Copyright (c) 1993 - 2004 Compugen Ltd.
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4 US-10-157-011-106
5 US-10-22-274-4
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4 US-10-278-481-2
4 US-10-278-481-3
4 US-10-278-481-13
4 US-10-278-481-13
4 US-10-278-481-15
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15 US-10-148-835-1
15 US-10-148-835-1
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Maximum Match 100%
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Sequence 8, Appli Sequence 3, Appli Sequence 10, Appli Sequence 2, Appli Sequence 10, Appli Sequence 1, Appli Sequence 2, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 17, Appli Sequence 11, Appli	ween protein and 530;	0; Gaps 0; SPAVMNYSIPS 60
v	reaction bet	6-254; 6-254; 7: Indels 0; Gaps 8:VUSHHEYPAMTFYSPAVMNYSIPS
US-10-148-835-8 US-10-148-835-3 US-10-148-835-14 US-10-148-835-10 US-09-933-267A-2 US-09-933-267A-2 US-09-933-267A-2 US-10-081-563-2 US-10-081-563-2 US-10-052-092-13 US-10-052-092-13 US-10-177-293-128 US-10-177-293-128 US-10-177-293-128 US-10-18-835-7 US-10-148-835-7 US-10-148-835-7 US-10-148-835-7 US-10-148-835-7 US-10-148-835-7 US-10-148-835-7 US-10-148-835-7 US-10-148-835-7 US-10-148-835-7 US-10-148-835-7 US-10-148-835-7 US-10-148-835-7 US-10-148-835-7 US-10-148-835-7 US-10-148-835-7 US-10-148-835-7 US-10-148-835-7 US-10-148-835-7 US-10-148-835-7 US-10-148-835-7 US-10-148-835-7 US-10-148-835-7 US-10-148-835-7 US-10-148-835-7 US-10-148-835-7 US-10-148-835-7 US-10-148-835-7 US-10-148-835-7 US-10-148-835-7 US-10-148-835-7 US-10-173-133-73	ALIGNMENTS 5 TD. ceting binding /198,785 -22044 -221963	Pred. No. 2.1 Pred. No. 2.1 0; Mismatches OSILPLEHGSIYIPS OSILPLEHGSIYIPS
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2000	SULT 1 -10-198-785-2 Sequence 2, Application US/1 Septence 2, Application US/2 GENERAL INPORMATION: APPLICANT: OLYMBYS OFTICAL, TITLE OF INVENTION: Method FILE REPERENCE: TEI-0280536 CURRENT APPLICATION NUMBER: 2 FRIOR FILING DATE: 2001-07- PRIOR APPLICATION NUMBER: 3 SOFTWARE: PALENTING NOW: 3 SOFTWARE: PALENTING NOW: 2.0 IENGTH: 530 TYPE: PRI TYP	Con 1 Similarity 530; Conser 1 MDIKNSPSS 1 MDIKNSPSS 1 MDIKNSPSS
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121 RETLKRKVSGNRCASPVTGPGSKRDAHFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGH

Db 301 LADKELVHMISWAKKIPGFVELSLFDQVRLLESCWAEVLAWSILFAPDL 360 Qy 361 VLDRDEGKCVEGILEIFPDMLATTSRFRELKLQHKEYLCVKAMILLNSSKYPLVTATQDA 420 Db 361 VLDRDEGKCVEGILEIFPDMLATTSRFRELKLQHKEYLCVKAMILLNSSKYPLVTATQDA 420 Qy 421 DSSRKLAHLLNAVTDALWWVIAKSGISSQQOSMRLANLLMLLSHVRHASNKGMEHLLNWK 480 Qy 421 DSSRKLAHLLNAVTDALWWVIAKSGISSQQOSMRLANLLMLLSHVRHASNKGMEHLLNWK 480 Qy 421 DSSRKLAHLLNAVTDALWWVIAKSGISSQQOSMRLANLLMLLSHVRHASNKGMEHLLNWK 480 Qy 481 CKNVVPVYDLLLEMLNAVTAKSGISSQQOSMRLANLLMLLSHVRHASNKGMEHLLNWK 480 Db 431 CKNVVPVYDLLLEMLNAVTAKSGISSQQOSMRLANLLMLLSHVRHASNKGMEHLLNWK 480 NBSULT 3 US-10-392-274-4 S GQUENCE 4, Application US/10392274 S FREULT 3 US-10-392-274-5 S FREULT 34 S PPDLICANT: AL-HENDY, AYMAN S APPLICANT: ADMSON, J. LARRY S APPLICANT: APPLICATION NUMBER: US/10/392, 274 CURRENT APPLICATION NUMBER: US/10/392, 274 S GOTWARRE PLILNC PATE: 2003-03-19 S MUMBER OF SEQ ID NOS: 6 S GOTWARRE: PATENT OF SEQ ID NOS: 6 S GOTWARRE: PATENT OF SEQ ID NOS: 6 S GOTWARRE: PATENT OF SEQ ID NOS: 6 S GORMANSM: HOMO SAPPIENS S TYPE: SRR	Duery Match 100.0%; Score 2805; DB 14; Length 530; Best Local Similarity 100.0%; Pred. No. 2.18-254; Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Duery Matches Duery Mismatches 0; Indels 0; Gaps 0; Duery Minimatches Duery Minimatches 0; Indels 0; Duery Minimatches Duery Minimatch
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Square 1, Application US/10373271

Publication No. US20030162257A1

Square Inforwarion:

GRURRAL INFORWARTION:

APPLICANT: Wyeth Staine M.

APPLICANT: Wyeth Emel

APPLICANT: Wyeth Staine M.

APPLICANT: Wyeth Staine M.

TITLE OF INVENTION: Variant

FILE RETERENCE: AM 00361

CURRENT APPLICATION WINBER: US/10/373,271

CURRENT APPLICATION WINBER: US/10/373,271

CURRENT PILING DATE: 2003-02-25

NUMBER OF SEQ ID NOS: 23

SOFTWARE: Patentin version 3.2

SEQ ID NO 1

LENGTH: 555
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                          RSIDHPCKLIFAPDLVLDRDEGKCVEGILEIFDMLLATTSRFRELKLQHKEYLCVKAMIL
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CRGANISM: human testis
CRGANISM: human testis
FRATURE:
NAME/KEY: misc feature
LOCATION: (534)
COTHER INFORMATION: Xaa can be any naturally occurring amino acid
FRATURE:
NAME/KEY: misc feature
LOCATION: (542)...(545)
COCATION: (542)...(545)
COCATION: (542)...(545)
US-10-373-271-1
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Best Local Similarity 92.4%;
Matches 477; Conservative
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CONTRY: Sweden
ZIP: S-14166
ZIP: S-14166
ZIP: S-14166
ZOMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IFIP PC compatible
COMPUTER: IFIP PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
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99.8%; Pred. No. 7.2e-231;
Live 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/278,481
FILING DATE: 23-OCT-2002
PRIOR APPLICATION NUMBER: US/09/333,057
FILING DATE: CURROWAN:
APPLICATION NUMBER: US/09/333,057
FILING DATE: CURROWAN:
APPLICATION NUMBER: GB 9518272.1
FILING DATE: 08-SEP-1995
APPLICATION NUMBER: GB 960550.4
FILING DATE: 11-APR-1996
APPLICATION NUMBER: GB 960550.4
FILING DATE: 11-APR-1996
APPLICATION NUMBER: GB 960550.4
FILING DATE: 11-APR-1996
APPLICATION NUMBER: GB 9609576.5
FILING DATE: 11-APR-1996
APPLICATION NUMBER: GB 9609576.5
FILING DATE: 11-APR-1996
                                                                                 Sequence 3, Application US/10278481
Publication No. US20030113803A1
GENERAL INFORMATION:
APPLICANT: KARO BIO AB
TITLE OF INVENTION: Orghan receptor
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: GUSTAFSCON, Jan-Ake
INFORMATION FOR SEG ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 485 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
ORIGINAL SOURCE:
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Matches 484, Conservative
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                                                                        US-10-278-481-3
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RESULT 7
US-10-278-481-13
Sequence 13. Application US/10278481
Sequence 13. Application No. UG20030113803A1
Publication No. UG20030113803A1
HAPLICANT: RARO BIO AB
TITLE OF INVENTION: Orphan receptor
NUMBER OF SEQUENCES: 19
STREET: c/o Center for Biotechnology and Department of Medical Mutrition, Karolinska Nutrition, Karolinska Institute
                                                                                                                                                                                                                                                                                                                            INSSMYPLVTATODADSSRKLAHLINAVTDALVWVIAKSGISSQQQSMRLANLLMLLSHV 465
                                                                                                                                                                                                                                                                          361 INSSMYPLASANQEAESSRKLTHLINAVTDALVWVIAKSGISSQQQSVRLANLLMLISH 420
                                                                                                                                                                                                                                                                                                                                                                                                        RHASNKGMEHLLAMKCKNVVPVYDLLLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSQ 525
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                                                                                                             241 SMPFTEASMMWSLTKLADKELVHMIGMAKKIPGFVELSILDQVRLLESCWMEVLMVGLMW 300
                                                                                                                                                                                                                                                   RSIDHPGKLIPAPDLVLDRDEGKCVEGILEIFDMLLATTSRPRELKLQHKEYLCVKAMIL 405
                                   SAPFIEASMMMSLIXLADKELVHMISWAKKIPGFVELSLPDOVRLLESCHMEVLAMGLMW
              CEGCKAPPKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLRKCYEVGMVKCGSRRBRCG
                                                                                          YRLVRRORSADEQLHCAGKAKRSGGHAPRVRRILLIDALSPEQLVLTLLEAEPPHVLISRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/333,057
FILING DATE: «Unknown»
APPLICATION NUMBER: 08/636,620
FILING DATE: «Unknown»
APPLICATION NUMBER: GB 9518272.1
FILING DATE: 08-82E-1995
APPLICATION NUMBER: GB 9605550.4
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
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FILING DATE: 23-OCC-2002
PRIOR APPLICATION DATE:
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ATTORNEY/AGENT INFORMATION:
NAME: GUSTAFSSON, Jan-Ake
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSSRKLAHLLNAVTDALVWVIAKSGISSQQOSMRLANLLMLLSHVRHASNKGWEHLLNWK 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: c/o Center for Biotechnology and Department of Medical Nutrition, Karolinska
                                         VLDRDEGKCVEGILEIFDMLLATISRFRELKLQHKBYLCVKAMILLNSSMYPLVTATQDA
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OPERATING SYSTEM: PC-DOS/MS-DOS
OPFRARE: Patent In Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,481
FILING DATE: 23-0ct-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 485,
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88.7%; Pred. No. 3.8e-206;
iive 23; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/333,057
FILING DATE: (Unknown)
APPLICATION NUMBER: 08/836,620
FILING DATE: (Unknown)
APPLICATION NUMBER: 08/81272.1
FILING DATE: 08-5EP-1995
APPLICATION NUMBER: GB 960550.4
FILING DATE: 15-WAR-1996
APPLICATION NUMBER: GB 960550.6
FILING DATE: 11-WAR-1996
APPLICATION NUMBER: GB 960576.5
FILING DATE: 08-WAY-1996
ATTORNEY, AGENT INFORMATION:
NAME: GUSTARESSON, Jan-Ake
INFORMATION FOR SEQ ID NO: 2.
                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/10278481
Publication No. US20030113803A1
GENERAL INFORMATION:
APPLICATION:
TITLE OF INVENTION: Orphan receptor
NUMBER OF SEQUENCES: 19
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SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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COUNTRY: Sweden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino
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Best Local S
Matches 430
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RESULT 9
US-10-278-481-14
is Sequence 14, Application US/10278481
spublication No. US2003113803A1
igeneration No. US2003113803A1
igeneration No. US2003103803A1
igeneration No. US2003103803A1
igeneration No. US2003103803A1
igeneration Number Of Sequence for Biotechnology and Department of Medical Nutrition, Narolinska Nutrition, Inc.
                                                                                                                                                                                                                                                                                                                                                              Length 485;
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88.0%; Pred. No. 6.8e-204;
tive 23; Mismatches 35;
  APPLICATION NUMBER: GB 960550.4
APPLICATION NUMBER: GB 960550.4
FILING DATE: 12-MAR-1996
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-AR-1996
APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
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                                                                                                                                                                                                                                                                                   ORGANISM: Mus musculus
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                  NAME: GUSTAFSSON, Jan-Ake
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                       LENGTH: 485 amino acids
TYPE: amino acid
TOPOLOGY: linear
ORIGINAL SOURCE:
                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 88.0%
Matches 427; Conservative
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US-10-278-481-5
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Sequence 5, Application US/10278481
Publication No. US20030113803A1
GENERAL INFORMATION:
APPLICANT: KARO BIO AB
TITLE OF INVENTION: Orphan receptor
NUMBER OF SEQUENCES: 19
STREET: c/o Center for Biotechnology and Department
of Medical Nutrition, Karolinska Nutrition, Karolinska
                                                                                                                                                                                                                                                                                                                                                                                                          421 RHISNKGMEHLLSMKCKNVVVVVVDLLLEMLNAHTLRGYKSSISGSECSSTEDSKNKRSSQ
                                                                                                                                                                             MIFYSPAVMYSVPGSTSNIDGGPVRLSTSPNVLWPTSGHLSPLATHCQSSLLYAEPQXS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
                                                                                                                    Indels
                                                                              Query Match 81.5%; Score 2286; DB 14;
Eest Local Similarity 88.6%; Pred. No. 1.1e-205;
Matches 429; Conservative 23; Mismatches 32;
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FILING DATE: «Unknown»
APPLICATION NUMBER: 08/836,620
APPLICATION NUMBER: 08/836,620
APPLICATION NUMBER: 08/836,620
APPLICATION NUMBER: 08/836,620
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) ORGANISM: Rattus rattus
) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-278-481-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Huddinge
COUNTRY: Sweden
ZIP: S-14186
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US-10-278-481-5
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                                                                                                                                                                                                                                                                                                              RSIDHPGKLIFAPDLVLDRDEGKCVEGILEIFDMLLATTSRFRELKLOHKEYLCVKAMIL
                                                                                                                                                                                                                                                                                                                               INSSMYPLVTATODADSSRKLAHLLNAVTDALVAVIAKSGISSOOOSMRLANLLMALSHV
                                                                                                 61 PWCEARSLEHTLPVNRETLKRKLGGSGCASPVTSPSTKRDAHFCAVCSDYASGYHYGVWS
                                                                                                                                          CEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRIRKCYEVGMVKCGSRRERCG
                                                                                                                                                                                                 YRLVRRORSADEOLHCAGKAKRSGGHAPRVRELLLDALSPEOLVLTLLEARPPHVLISRP
                           46 MTFYSPAVMAYSIPSNVTNLEGGPGRQTTSPNVLMPTPGHLSPLVVHRQLSHLYABPQXS
                                            106 PWCEARSLEHTLPVNRETLKRKVSGNRCASPYTGPGSKRDAHFCAVCSDYASGYHYGVWS
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TOPOLOGY: linear
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ZIP: S-14186
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: TBM FC COMPATIBLE
COMPUTER: Parent IN Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,481
FILING DATE: 23-OCT_2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 484;
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Best Local Similarity 88.0%; Pred. No. 2e-203;
Matches 426; Conservative 23; Mismatches 35;
                                                                                                                                                      PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/333,057
FILING DATE: «Unknown»
APPLICATION NUMBER: 08/836,620
FILING DATE: «Unknown»
APPLICATION NUMBER: 08 951872.1
FILING DATE: 08-5EP-1995
APPLICATION NUMBER: GB 960550.4
FILING DATE: 15-WAR-1996
APPLICATION NUMBER: GB 9609576.5
FILING DATE: 1-WAR-1996
APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-WAY-1996
ATTORNEY/AGENT THORPAMATION:
NAME: GUSTAFESSON, Jan-Ake
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Mus musculus
SEQUENCE DESCRIPTION: SBQ ID NO: 14:
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TYPE: amino acid
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EQLVLTLLEARPPHYLISRPSAPFTRASMMSLTKLADKELVFMISWAKKIPGFVELSLF 325
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RESULT 10
US-10-278-481-15
Sequence 15, Application US/10278481
Sequence 15, Application Wo. US20030113803A1
SENBRAL INFORMATION:
APPLICANT: KARO BIO AB
ITTLE OF INVENTION: Orphan receptor
INVERE OF SEQUENCES: 19
STREET: c/o Center for Biotechnology and Department of Medical Nutrition, Karolinska
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86 LSPLVVERQLSHLYABPQKSPWCBARSLEHTLPVNRETLKRKVSGNRCASPVTGPGSKRD
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                                                                                                                                                                                                                                                                                                                CITY: Huddinge
CCUNTRY: Sweden
ZIP: S-14186
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 384;
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71.9%; Score 2017; DB 14;
Best Local Similarity 100.0%; Pred. No. 1.5e-180;
Matches 383; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA

TOTAL APPLICATION NUMBER: US/10/278,481

PILING DATE: 23-0ct-2002

PRIOR APPLICATION NUMBER: US/09/333,057

PILING DATE: «Uhknown»

APPLICATION NUMBER: US/09/333,057

PILING DATE: «Uhknown»

APPLICATION NUMBER: GB 95.8272.1

PILING DATE: 10-8EP-1996

APPLICATION NUMBER: GB 960550.4

PILING DATE: 11-APR-1996

APPLICATION NUMBER: GB 960732.0

PILING DATE: 11-APR-1996

APPLICATION NUMBER: GB 9609576.5

PILING DATE: 11-APR-1996

APPLICATION NUMBER: GB 9609576.5
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ORAGAISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-278-481-15
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61 NVINLEGGEGRO-----TTSPNVLWPTPGHLSP-LVVHROLSHLYAR 101
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                                                                                                                                                                                                                                   RESULT 11
US-10-146-035-5
US-10-146-035-5
Sequence 5, Application US/10148035
Publication No. US20030207380A1
GENERAL INFORMATION:
APPLICANT: SAITOR
TITLE OF INVENTION: MUTANT BR alpha AND TEST SYSTEMS FOR TRANSACTIVATION
FILE REFREENCE: 218-0648P
CURRENT APPLICATION NUMBER: US/10/148,835
CURRENT FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 213
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S NSPSSINSPSSYNCSQSILPLEH--GSIYIPSS--YVDSHHEYPAMTFYSPAVMVYSIPS
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al Similarity 48.4%; Pred. No. 8.2e-107;
264; Conservative 88; Mismatches 128;
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US-10-148-835-5
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LENGTH: 595
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Matches 264
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Publication No. US20030207380A1
GENERAL INFORMATION:
APPLICANT: SAITO et al.
TITLE OF INVENTION: MUTANT ER Alpha AND TEST SYSTEMS FOR TRANSACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 NELEPLARP-----QLKIPLERPLGEVYLDSSKPAVYNYPEGAAYENAAAANAQVYG
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US-09-853-033-2
; Sequence 2, Application US/09853033
; Patent No. US202020100068A1
; Patent No. US202020100068A1
; GENERAL INPORMATION:
APPLICANT: CHAMEDAN: PIERRE
APPLICANT: METGER, DANIEL
; TITLE OF INVENTION: MEDIATED BY MODIFIED CRE-ER
; TITLE OF INVENTION: MEDIATED BY MODIFIED CRE-ER
; TITLE OF INVENTION: MEDIATED BY MODIFIED CRE-ER
; TITLE OF INVENTION UNMBER: US/09/853,033
; CURRENT APPLICATION NUMBER: US/09/853,033
; CURRENT PILLING DATE: 2001-05-11
; PRIOR PILLING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 14
; NUMBER OF SEQ ID NOS: 14
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48.4%; Pred. No. 1.3e-106;
ive 88; Mismatches 128;
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Matches 264; Conservative
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US-09-853-033-2
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LENGTH: 595
TYPE: PRT
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TTLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION FILE REFERENCE: 218 CURRENT APPLICATION NUMBER: US/10/140,835
CURRENT APPLICATION BATE: 2002-10-11
NUMBER OF SEQ ID NOS: 213
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 Q-TGLPYGPGSEAAAFGSNGLGGFPPLNSVSPSPLMLHPPPQLSPFLQPHGQVPYYLB
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48.4%; Pred. No. 1.3e-106;
.ive 88; Mismatches 128; Indels
FILE REFERENCE: 2185-0648P
CURRENT APPLICATION NUMBER: US/10/148,835
CURRENT FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 213
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 48.4% Matches 264; Conservative
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-835-2
                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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US-10-148-835-1
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Sequence 9, Application US/10148835

Publication No. US20030207380A1

GENERAL INFORMATION:

APPLICAT: SAITO et al.

TITLE OF INVENTION: WUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION

TITLE OF INVENTION: 2185-0648P

CURRENT APPLICATION NUMBER: US/10/148,835

CURRENT PILNG DATE: 2002-10-11

NUMBER OF SEQ ID NOS: 213

SOFTWARE: Patentin Ver. 2.0

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                            21 NELEPLMRP-----QLKIPLERPLGEVYLDSSKPAVYNYPEGAAYEFNAAAANAQVYG
                                                                                                                                                         61 NVTNLEGGPGRQ------TTSPNVLMPTPGHLSP-LVVHRQLSHLYAB
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Length 595;
/ Match 123.5; DB 15; Lengt Local Similarity 48.4%; Pred. No. 1.3e-106; les 264; Conservative 88; Mismatches 128; Indels
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44.0%; Score 1233.5; DB 15

Best Local Similarity 48.4%; Pred. No. 1.3e-106;

Matches 264; Conservative 88; Mismatches 128;
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, ORGANISM: Homo sapiens
US-10-148-835-9
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215 VKCGSRRERCGYRLVRRQRSADEQLHCACKAKRSGGHAPRVR------EL 258 :| | :| | :| | | :| | | 251 MKGGIRKDRRGGRMLKHRRQRDD-----GEGRGEVGSAGDMRAANLWPSPLMIKRSKKNS 305
                                                                                                            134 NEPŠGYTVRĒĀGPPAFYRP---NSDNRRQGGRERLASTNDKGSMAMESAKETRYCAVCND 190
75 Q-TGLPYGPGSBAAAPGSNGLGGPPPLMSVSPSPLMILHPPPQLSPFLQPHGQQVPYYLE 133
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Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model

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Run on:

June 20, 2004, 10:30:42; Search time 59 Seconds (without alignments) 2538.139 Million cell updates/sec

US-08-906-365-2 2805 1 MDIKUNSPSSILNSPSSYNCSQ.......ECSPAEDSKSKEGSQNPQSQ 530 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 surmaries

A Geneseq 29Jan04:*

1: geneseq11980s:*

2: geneseq12000s:*

4: geneseq22001s:*

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6: geneseq2203s:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SIIMMARIES

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SUMMAKIES	ID	AAW33215	AAW97858	AAB60649	AAU27322	AAE10457	AAB47835	ABG32754	ADA83824	ABU61628	ADE12138	AAY07270	ABB80756	AAW14724	AAY01597	AAW33212	AAB47834	AAW98125	AAY04434	ABJ72350	AAW98128	AAY04433	AAW14723	AAY01596	AAW14725	AAW98126
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ALIGNMENTS

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This sequence represents a novel oestrogen binding protein isolated from human testis cDNA in order to study upstream translation-initiation codons using 5' RACE-PCR technology. This receptor is able to bind and be activated by estradiol, estone and estriol, can be used in a screening assay for the identification of new drugs e.g. novel ligands or hormonal analogues
                                                                                                                                                                                                                                                                                                                                                                         DNA encoding estrogen receptor - useful in screening assay to identify novel ligands or hormonal analogues.
                                                                                                 Oestrogen receptor protein, steroid, alternative splicing, estradiol, estone, estriol, screening.
                                                                           Human oestrogen receptor protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 35-37; 45pp; English.
AAW33215 standard; protein; 530 AA.
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96EP-00203284
                                                    20-APR-1998 (first entry)
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N-PSDB; AAT88415.
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22-NOV-1996;
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Sequence 530 AA;

ô Gaps ö Length 530; Indels Query Match
100.0%; Score 2805; DB 2;
Best Local Similarity 100.0%; Pred. No. 2.4e-258;
Matches 530; Conservative 0; Mismatches 0;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human oestrogen receptor-beta coding sequence - useful in the production of human oestrogen receptor-beta and identification of human oestrogen receptor-beta interactive compounds.
                                                                                                            361 VLDRDEGKCVEGILEIFDMLLATTSRFREEJTQHKEYLCVKAMILLNSSMYPLVTATQDA
                 MDIKNSPSSLNSPSSLNSPSSYNCSQSILPLEHGSIYIPSSSYNDSHHEYPAMTFYSPAVMYYSIPS
                                         NVTINLEGGPGRQTTSPNVLWPTPGHLSPLVVHRQLSHLYAEPQKSPWCEARSLEHTLPVN
                                                                           RETLIKRIVSGNRCAS PVTGPGSKRDAHFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGH
                                                                                      121 RETLKRKVSGNRCASPVTGPGSKRDAHFCAVCSDYASGYHYGVWSCEGGKAPFKRSIQGH
                                                                                                                                               CAGKAKRSGGHAPRVRELLLDALSPEQLVITLLEAEPPHVLISRPSAPFTEASMMMSLTK
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        MDIKNSPSSLNSPSSYNCSQSILPLEHGSIYIPSSYVDSHHEYPAMTFYSPAVMYSIPS
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                                                                                                                                                                                                                                                                                                                                                                                                                      Oestrogen receptor-beta; hER-beta; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 17; Page 42-44; 49pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hsiao C,
                                                                                                                                                                                                                                                                                                                                                  AAW97858 standard; protein; 530
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N-PSDB; AAX24364,
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This polypeptide comprises a full-length human oestrogen receptor-beta (hRR-beta), including 45 previously unknown N-terminal amino acid residues that are believed to contribute to the transcription activation function of the receptor. The amino acid sequence was deduced from the mucleotide sequence (see AAX24364) of an isolated cDNA clone. hER-beta is selectively expressed in the thymus, spleen, overy and testes. The invention encompasses hER-beta polymucleotides and polypeptides, particularly peptides which include residues 1-45 of hER-beta. The invention also provides expression systems in which transcriptionally active hER-beta or fragments can be produced, as well as screening methods for identifying hER-beta agonists and antagonists (including tissue-specific oestrogens and anti-oestrogens), and hER-beta co-activators and inhibitors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 2.4e-258;
Matches 530; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ¥.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 530 AA;
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DSSRKLAHILINAVTDALVWVIAKSGISSQQQSMRLANLLMLLSHVRHASNKGMEHLLINMK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 4; 245pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hwang SS,
                                                                                                                                                                      AAU27322 standard; protein; 530
                                                                                                                                                                                                                                                                  Human Oestrogen receptor beta.
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                                                                                                                                                                                                                                   18-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kalush F, Cassel MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-582041/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PEKE ) PE CORP NY
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                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method for examining the interaction of a test substance with a hormone receptor protein. The method involves contacting a test substance with a hormone receptor protein (e.g., an oestrogen receptor) which is labelled with an optical marker (e.g., a fluorescent protein), where the marker is capable of undergoing a change in its optical properties when the receptor binds a ligand. The optical signal generated in the presence of the test compound is then compared with that test compound is interacting with the hormone receptor protein. The invention also encompasses the labelled hormone receptor protein, the method of the invention is used for the investigation and diagnosis of hormonal disorders, especially those associated with sex hormones egg., suppression of ovulation. The present sequence represents human oestrogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 RETLXRKVSGNRCASPVTGFGSKRDAHFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Determination of the interaction of a substance for investigation and diagnosis of hormonal disorders using an optically labelled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MDIKNSPSSLNSPSSYNCSQSILPLEHGSIYIPSSYVDSHHEYPAMTFYSPAVMNYSIPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGKAKRSGGHAPRVRELLLDALSPEQLVITLLEAEPPHVLISRPSAPFTEASMMMSLTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 530;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 2805; DB 4;
Pred. No. 2.4e-258;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                             Claim 26; Page 68-72; 75pp; Japanese.
                                                                                                                                                     (OLYU ) OLYMPUS CPTICAL CO LTD.
                                                                                        23-JUL-1999; 99JP-00209860.
31-MAY-2000; 2000JP-00163475.
31-MAY-2000; 2000JP-00163476.
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                                                           24-JUL-2000; 2000WO-JP004930
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Best Local Similarity 100.
Matches 530; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor beta (ER-beta)
                                                                                                                                                                                     Kato N;
                                                                                                                                                                                                                  WPI; 2001-168581/17.
                                                                                                                                                                                                                                   N-PSDB; AAF59897
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WO200107919-A1.
                                                                                                                                                                                     Sakamoto H,
                               01-FEB-2001
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The invention relates to a novel isolated peptide comprising or consisting of an amino acid sequence selected from an amino acid sequence selected from an amino acid sequence consisting of an amino acid sequence selected from an amino acid sequence of a variant oestrogen receptor protein (e.g. ERbeta), or a fragment of namino acids), antibodises against them, incisic acids encoding them (including vectors for transforming cells). The gene for human ERbeta is located on chromosome 64.25.1. The variant sere encoded by single or uncleotide polymorphisms (SNP). The variant peptides and proteins can be compounded to determine the biological activity of the protein, to raise antibodies, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, to identify compounds that modulate receptor activity and to streen compounds for the antibody can be used to isolate the receptor protein and a target molecule that normally interacts with the receptor protein and a target molecule that normally interacts with the receptor protein cases expression in disease states e.g. cardiovascular disease and autoimmune disease (e.g. systemic lupus erythematosus, arthritis, cheumatism and osteoarthritis), osteoporososis, breast cancer and endomerrial cancer. In addition the antibodies can be used in pharmacogenomic analysis and inhibiting protein function, e.g. blocking the bidming partners such as a ligand. The nucleic acids encoding the proteins can be used as the probes, primers, chemical intermediates and in biological assays. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, Oestrogen receptor beta; ERbeta; SNP; chromosome 6q.25.1;
single nucleotide polymorphism; cardiovascular disease;
autoimmune disease; systemic lupus erythematosus; arthritis; rheumatism;
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DSSRKLAHILINAVTDALVWVI AKSGISSQQQQRIKLANLLMILSHVRHASNKGMBHLINMK
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                                                                                                                                                        530
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ER-beta-regulated gene expression.

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candidate compound and detecting
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                                              Example 3; Fig 7A; 49pp; English
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Best Local Similarity 100.
Matches 530; Conservative
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                                                                                                                MDIKONSPSSINSPSSYNCSQSILPLEHGSTYIPSSYVDSHHEYPAMTFYSPAVMVSIPS
                                                                                                                                                            NVTNLEGGPGRQTTSPNVLMPTPGHLSPLVVHRQLSHLYASPQKSPWCEARSLEHTLPVN
                                                                                                                                                                                                NVTNLEGGPGRQTTSPNVLWPTPGHLSPLVVHRQLSHLYABPQKSPWCEARSLEHTLPVN
                                                                                                                                                                                                                                                                NDYICPATNOCTIDKNRRKSCQACRIRKCYEVGMVKCGSRRERCGYRLVRRQRSADEQLH
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                                                                                                                                                                                                                                                                                                                                                                                                     CAGKAKRSGGHAPRVRELLLDALSPEQLVLTLLEAEPPHVLISRPSAPFTEASMMSLTK
                                                                                MDIKNSPSSINSPSSYNCSQSILPLEHGSIYIPSSYVDSHHEYPAMTFYSPAVMYSIPS
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      Length 530;
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                                            Indels
Query Match
100.0%; Score 2805; DB 4;
Best Local Similarity 100.0%; Pred. No. 2.4e-258;
Matches 530; Conservative 0; Mismatches 0;
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The invention relates to in vitro screening for modulator of estrogen receptor-beta (RR-beta)—rediated cell growth inhibition. The method involves contacting mammalian cell having functional ER-beta protein with candidate compound and detecting increase/decrease of ER-beta regulated gene expression in presence of candidate compound compared to expression in absence of the compound. The method is useful for identifying a compound that modulates ER-beta-mediated cell growth inhibition. It is useful for testing dietary compounds, e.g. red wine, for the presence of physiological function positively or negatively and for testing physiological function positively or negatively and for testing environmental pollutants for the presence of estrogen minics that may pose health risks involving ER-beta-mediated processes. The present sequence is human ER-beta mediated processes. The present
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100.0%; Pred. No. 2.4e-258;
ive 0; Mismatches 0;
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scientific research
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                                                                                                                                                                                                                                                                                                                                                                                    dditional N-terminal sequences of this sequence, compared to the ER sequence given in AAB4784, were generated using RACE PCR. The gene encoding this new ER is located on chromosome 14 and has a different tissue distribution from classical ER. This ER also has two orphan ER's, ER-alpha and ER. Deta. These orphan receptors have estrogen receptor related structure but do not appear to able to bind estradiol or other ER ligands. The DNA binding domain (DBD) and ligand binding domain (LBD) from this ER may be used in the chimeric receptor, or DNA encoding it, is useful in a screening assay for identification of new drugs. Similar chimeric receptors comprising the LBD of the machiner nuclear receptor of the DDD and a comprising the DDD and or the Standard Compounds to it is useful in a screening decived from another nuclear receptor e.g., progesterone receptor, are useful for the screening of compounds to identify new ligands or hormone analogs which are able to activate the new ER. Chimeric receptors comprising are new ER. Chimeric receptors comprising as the comprising of the new ER. Chimeric receptors comprising and an N-terminal domain derived from another nuclear receptor.

N-terminal domain derived from another nuclear receptor.
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                                                                                                                                                                                                                                                                                         New isolated chimeric receptor comprising a DNA binding domain and/or ligand binding domain of a new estrogen receptor, for identifying functional ligands or hormonal analogs for the receptor.
                                                                                                                                                                                                                                                                                                                                                                            sequence shows the full length novel estrogen receptor (ER). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   identify new ligands or hormone analogs for the nuclear receptors
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estradiol; nuclear receptor; progesterone receptor.
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100.0%; Pred. No. 2.4e-258;
ive 0; Mismatches 0;
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                                                                                                          25-MAR-1997, 2001EP-00202021.
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97EP-00200903.
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N-PSDB; AAI72144.
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22-NOV-1996;
25-MAR-1997;
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                            Homo sapiens.
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This invention relates to a novel isolated nucleic acid molecule coding for a cofactor of the oestrogen beta nuclear receptor. The proteins of the invention may have osteogathic, cytostatic, antiarteriosclerotic, contropic, neuroprotective and cardiant activity. The nucleic acid molecule is useful for encoding a cofactor of the cestrogen beta nuclear receptor which mediate estrogen receptor transactivation activity and chus, provide means for the treatment of numerous diseases such as the cancer, cardiovascular diseases, failures in reproductive functions, cancer, cardiovascular diseases uch as atherosclerosis as well as the prevention of hot flushes, mood changes and Alzheimer's disease. The cofactor proteins are also useful in screening for ligands of the cestrogen receptor beta, in screening drugs for agonist and antagonist activity, and as scientific research tools, e.g. for developing nucleic activity, and as scientific research tools, e.g. for developing nucleic activity, and as uninimitied for the detection of these proteins. Methods of the invention are useful for developing and identifying compounds for the treatment of the above diseases. The present sequence represents the
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                                                                                                                                                                                                                                 New nucleic acid molecule encoding cofactor (CF) 13, CF14 or CF15 of estrogen beta nuclear receptor for treating diseases, e.g. osteoporosis, cancer, atherosclerosis or Alzheimer's disease, screening assays and
                                                   361 VLDRDEGKCVEGILEIPDMLLATTSRFRELKLQHKEYLCVKAMILLNSSMYPLVTATQDA
                                                                                                                                                                             421 DSSRKLAHLLNAVTDALVWVIAKSGISSQQQSMRLANLLMLLSHVRHASNKGMEHLLNMK
361 VLDRDEGKCVEGILEIFDMLLATTSRFRELKLQHKEYLCVKAMILLNSSMYPLVTATQDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; nuclear receptor oestrogen beta; osteopathic; cytostatic; antiarteriosclerotic; nootropic; neuroprotective; cardiant; cancer; osteoporosis; bone disease; reproductive disorder; atherosclerosis; cardiovascular disease; Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                          CKNVVPVYDLILEMINAHVIRGCKSS ITGSECSPAEDSKSKEGSQNPQSQ
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16-MAY-2001; 2001EP-00111862.
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RETLIKRKVSGNRCASPVTGPGSKRDAHFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGH 180
 invention
                                                                                                                    1 MDIXNSPSSLNSPSSYNCSQSILPLEHGSIYIPSSYVDSHHEYPAMTFYSPAVMNYSIPS
                                                                                                                                           1 MDIKNSPSSLNSPSSYNCSQSILPLEHGSIYIPSSYVDSHHEYPAMTFYSPAVMYSIPS
                                                                                                                                                                                     NVTNLEGGPGROTTSPNVLWPTPGHLSPLVVHRQLSHLYAEPQKSPWCBARSLEHTLPVN
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                                                            Length 530;
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nuclear receptor protein (ER beta)
                                                          100.0%; Score 2805; DB 5;
100.0%; Pred. No. 2.4e-258;
ive 0; Mismatches 0;
                                                                                         Conservative
human oestrogen beta
                                                                          Similarity
                            Sequence 530 AA;
                                                       Query Match
Best Local Simi
Matches 530;
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240 240 180 300 CAGKAKRSGGHAPRVRELLLDALSPBQLVLTLLRAEPPHVLISRPSAPFTEASMMSLTK 300 NDYI CPATNOCTI DKNRRKSCQACRLRKCYBVGMVKCGSRRERCGYRLVRRQRSADEQLH 191 NDYICPATNQCTIDNONRRKSCQACRLRKCYBVGAVXCGSRRBRCGYRLVRRQRSADEQLH CAGKAKRSGGHAPRVRBLLLDALSPRQLVLTLLBABPPHVLISRPSAPFTBASMMSLTK 181

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360 360 420 LADKELVHMISWAKKIPGFVELSLFPQVRLLESCWMEVLAMGLAMKSIDHPGKLIPAPDL LADKELVHMISWAKKI PGFVELSLFDQVRLLESCWMEVLMMGLMWRSIDHPGKLIFAPDL VLDRDEGKCVBGILEI FDMLLATTSRPRELKLQHKBYLCVKAMILLNSSMYPLVTATQDA 301 301

480 VLDRDEGKCVEGILEIFDMLLATTSRFRELKLQHKEYLCVKAMILLINSSMYPLVTATQDA DSSRKLAHLLNAVTDALVWVIAKSGISSQQSMRLANLLMLLSHVRHASNKGMEHLLNMK DSSRKLAHLLNAVTDALVWVIAKSGISSQQQSMRLANLLMLLSHVRHASNKGMEHLLNMK 361 421 421

ADA83824 standard; protein; 530 ADA83824

20-NOV-2003

Human ESR2 protein

expressed sequence tag; EST; arabidopsis; tumour; phenotype; hyperosmotic stress; colon cancer; immunogen; human; marker; e stress-induced p vaccine.

Homo sapiens.

27-DEC-2002.

WO2002103028-A2

30-MAY-2002; 2002WO-IB004189

30-MAY-2001; 2001US-0293999P. 22-OCT-2001; 2001US-0330457P. 19-FEB-2002; 2002US-0357144P. 30-MAY-2001;

BIOM- BIOMEDICAL

530

CKNVVPVYDLILEMINAHVIRGCKSSITGSECSPAEDSKSKEGSONPQSQ CKNVVPVYDLILEMINAHVIRGCKSSITGSECSPAEDSKSKEGSONPOSO

481

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17 Krukovskaya ΑV Lobashev Kozlov AP, NK, Yankovsky 2003-175241/17. AV,

Determining if a nucleic acid is a marker for a phenotype/cell type of interest, by global comparison of expressed sequence tags known to be expressed in the phenotype/cell type with all ESTs expressed in normal

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120

60

Claim 29; Page 217-220; 516pp; English

The invention relates to a novel method for determining if a nucleic acid is a marker for a predetermined phenotype/cell type of interest from a comparison of a group of expressed sequence tags (ESTS) known to be expressed in the phenotype/cell type of interest with all ESTs expressed in normal tissue comparison of a group of expressed sequence tags (ESTS) known to be expressed in the composition of the invention is useful for the comparison of the invention is useful for determining whether a nucleic acid is a marker for a predetermined phenotype or cell type of interest from a biological species, preferably as a tumour cell, and the predetermined phenotype is a stress induced to henotype such as hyperosmotic stress or high salt conditions. A method of the invention is also useful for detecting a tumour cell, and for regulating or cancer in a human, for detecting a tumour cell, and for regulating or preventing the growth of a tumour cell. An antibody of the invention is useful for detecting a tumour cell. An antibody of the invention is tumour-associated markers. A polypeptide of the invention is useful as an immunogen for vaccinating an animal. The present sequence represents a tumour-associated markers.

Sequence 530 AA;

420 480

530

CKNVVPVYDLLLEMINAHVLRGCKSSITGSECSPARDSKSKEGSQNPQSQ 530

CKNVVPVYDLLLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSONPOSO

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                                                                                                                                                     61 NYTNLEGGEGGTGTTSPNVLMPTPGHLSPLVVHRQLSHLYAEPQKSPWCEARSLEHTLPVN 120
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Length 530;
                               Indels
 Query Match
100.0%; Score 2805; DB 6;
Best Local Similarity 100.0%; Pred. No. 2.4e-258;
Matches 530; Conservative 0; Mismatches 0;
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us-08-906-365-2.rag

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The invention relates to detecting the presence/absence of binding capacity of a test substance, with respect to a protein, involves having a protein, which has been labeled with fluorescence material, exist in a colution and while successively measuring fluorescence intensity from the fluorescent material, reacting the test substance with labeled protein and determining binding capacity of the test substance, with respect to protein, on basis of successive change in fluorescent intensity. Also involving construction an expression vector by incorporating a gene encoding the protein, and a prometer for expression vector by incorporating a gene conding the protein, and a prometer for expression vector by incorporating a gene conding the protein, and a prometer for expression vector by incorporating a gene coroting the protein, and a prometer for expression vector by incorporating a gene coroting the protein, as a hormone receptor (e.g. an obstrugen of the protein, thus producing the protein labeled with the fluorescent material. The protein as a hormone receptor (e.g. an obstrugen of a lest substance to a receptor (e.g. an obstrugen receptor) antigen or antibody. The method is useful for detecting a binding of a rest substance to a receptor, by maintaining a receptor (which has been labeled with a marker material capable of generating a complex and this receptor/ligand complex on it, in a solution in which the receptor and the ligand can form a complex and this receptor/ligand complex can be bound to the complex. The presence/absence of the receptor/rest substance/nucleic acid fragment having the specific nucleic acid sequence, in which the receptor/ligand fragment complex is detected by measuring diffusion in the, in the complex is detected by measuring diffusion in the intensity of the labeled receptor. The measurement is performed by distribution analysis (FIDA). The receptor/ligand complex and encoding an uncleic acid fragment having the specific nucleic acid fragment having the specific nucleic acid fragment
                                                                                                                                                                                                                Human; oestrogen receptor beta; hER beta; receptor; FCS; FIDA;
fluorescence correlation spectroscopy; green fluorescent protein; GFP;
fluorescence intensity distribution analysis; nuclear receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting binding capacity of test substance, with respect to a py reacting test substance with fluorescence-labeled protein and detecting change in the fluorescence intensity.
                                                                                                                                                                           Human oestrogen receptor beta, hERbeta
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                                          ABU61628 standard; protein; 530 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (OLYU ) OLYMPUS OPTICAL CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JUL-2001; 2001JP-00220444.
23-JUL-2001; 2001JP-00221963.
                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUL-2002; 2002US-00198785.
                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                    ABU61628;
RESULT 9
ABU61628
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amount of the receptor monomer and the amount of the receptor/test substance/nucleic acid fragment complex with relative values. The nucleic acid is DNA. The detection is carried out according to high-throughput detection. The present sequence represents human oestrogen receptor beta (hBRDeta) which is coupled to green fluorescent protein (GFP) and used in the method of the invention
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oestrogen-dependent genitourinary condition; leiomyoma; fibroid;
pregnancy prevention; gynaecological; cytostatic; contraceptive;
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                                                                                                                        100.0%; Score 2805;
100.0%; Pred. No. 2.4
ive 0; Mismatches
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                                                                                                                                                    Conservative
                                                                                                                                        Similarity
                                                                                                Sequence 530 AA;
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Euman; oestrogen receptor; ligand; bone resorption; metabolic disorder; cardiovascular disease; cancer; central nervous system; breast; uterine; osteoporosis; ovarian; prostate; diabetes; Alzheimer's disease.
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                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 1; 32pp; English.
                                               oestrogen receptor
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N-PSDB; AAX34309.
                                                                                                                                                                                                                                                                                (MERI ) MERCK
                                                                                                                     Homo sapiens
                                                                                                                                             WO9912961-A1
                                                                                                                                                                                                                  08-SEP-1997;
30-SEP-1997;
30-OCT-1997;
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                      06-JUL-1999
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                                                                                                                Treating an estrogen-dependent genitourinary condition in a patient by administering to the patient an expression construct comprising a mucleic acid sequence encoding a modified estrogen receptor e.g., leiomyoma or fibroid.
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                                                                                                                                                                                                    The invention relates to a method for treating an oestrogen-dependent genitourinary condition in a patient comprising administering an expression construct comprising a nucleic acid sequence encoding a modified oestrogen receptor. The sequence is under the control of a promoter. The method is useful for treating an oestrogen-dependent genitourinary condition in a patient, e.g., leiomyoma or fibroids, or preventing pregnancy. This sequence represents the human oestrogen receptor beta polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                         MDIKNSPSSLNSPSSYNCSQSILPLEHGSIYIPSSYVDSHHEYPAMTFYSPAVMYSIPS
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                                                                                                                                                                                                                                                                                                                                         ; Score 2805; DB 7;
; Pred. No. 2.4e-258;
0; Mismatches 0;
                                                                                                                                                                                Claim 27; SEQ ID NO 4; 46pp; English
                                                            Jameson JL;
                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%;
Best Local Similarity 100.0%;
Matches 530; Conservative 0;
19-MAR-2002; 2002US-0365760P.
                       (TEXA ) UNIV TEXAS SYSTEM (NOUN ) UNIV NORTHWESTERN
                                                          Lee EJ,
                                                                                  WPI; 2003-852811/79
                                                                                               N-PSDB; ADE12137
                                                                                                                                                                                                                                                                                                                    Sequence 530 AA;
                                                          Al-Hendy A,
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97US-0058271P. 97US-0060520P. 97GB-00022884. 98GB-0006032.

& CO INC

98WO-US018577

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This sequence represents a human oestrogen receptor. The receptor can be used to identify ligands that bind to human oestrogen receptor. The ligands can be used in a method for preventing or treating an oestrogen receptor mediated disease or condition, such as abnormal bone resorption, a cardiovascular disease, cancer, metabolic disorders, or central nervous system disorders. The ligand is especially used to treat osteoporosis, breast, uterine, ovarian or prostate cancer, diabetes or Alzheimer's
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100.0%; Pred. No. 2.5e-258;
ive 0; Mismatches 0;
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les 530; Conservative
                                                                                                                                                                                                                                                       Sequence 548 AA;
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548

standard; protein;

AAY07270

RESULT 11
AAYO7270
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AAW14724;
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                         438
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                                                                  DSSRKLAHLLNAVTDALVWVIAKSGISSQQQSMRLANLLMELSHVRHASNKGMEHLLNMK
  VLDRDEGKCVEGILEIFDMLLATTSRFRELKLQHKEYLCVKAMILLNSSMYPLVTATQDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Autocorrection function-embedded confocal optics-based fluorometric analyzers for studying behaviors of fluorescence-labeled molecules particularly intracellular biological molecules like proteins at
                                                                                                                                                                                                                                                                                                     Fluorometric analyzer, laser, fluorescence, GFP, ER beta, human, g
green fluorescent protein, estrogen receptor beta, fusion protein.
                                                                                                        CKNVVPVYDLLLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSQNPQSQ 530
                                                                                                                    CKNVVPVYDLILEMINAHVIRGCKSSITGSECSPAEDSKSKEGSQNPQSQ 548
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No. 4.4e-258;
                                                                                                                                                                                                                                                                             acid sequence of a fusion GFP/hBR beta protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Page 98-105; 109pp; Japanese.
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Pred.
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N-PSDB; ABN86125.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                              Synthetic.
Aequorea victoria.
Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                  WO200248693-A1.
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                         1 MDIKNSPSSINSPSSYNCSQSILPLEHGSIYIPSSYVDSHHEYPAMTFYSPAVMNYSIPS
                                                                           NVTINLEGGPGROTTSPNVLWPTPGHLSPLVVHROLSHLYAEPOKSPWCEARSLEHTLPVN
                                                                                                                                                                                   NDYI CPATNOCTI DIOMRRKS COACRIRKCY BY GWYKCGSRRERCGYRLVRRORS AD BOLH
                                                                                                                                                                                                                                      CAGKAKRSGGHAPRVRELLLDALSPEQLVLTLLEAEPHVLISRPSAPFTEASMMSLTK
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Gaps
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/label= DNA-binding_domain
260. .45/
/label= Ligand-binding_domain
 Mismatches
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96GB-00005550.
96GB-00007532.
96GB-00009576.
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    530; Conservative
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15-MAR-1996,
11-APR-1996,
08-MAY-1996;
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disease

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The present sequence represents an estrogen receptor-beta. The specification describes a method for screening test compounds for differential estrogen receptor (ER) alpha-mediated and ER beta-mediated activation at an API after. The method is used for identifying compounds which can be used in therapy
                           estrogen receptor; ER-alpha; ER-beta; activation; AP1 site;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RSIDHPGKLIFAPDLVLDRDEGKCVBGILEIFDMLLATTSRFRELKLQHKEYLCVKAMIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 PWCEARSLGHTLPVNRETLKRKVSGNRCASPVTGPGSKRDAHFCAVCSDYASGYHYGVWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YRLVRRQRSADBQLHCAGKAKRSGGHAPRVRBLLLLDALSPBQLVLTLLBABPPHVLISRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MTFYSPAUMNYSI PSINUTINLEGGPGRQTTSPINULWPTPGHLSPLVVHRQLSHLYABPQKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Screening for test compounds which inhibit or activate estrogen recep
beta (ER-beta) mediated activation at a AP1 site - for use in therapy
                                                                                                                                                                                                                                                                       Nilsson S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 2535; DB 2;
Pred. No. 1.2e-232;
0; Mismatches 4;
                                                                                                                                                                                                                                                                       Kuiper GGJM,
                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 14; Page 43-44; 61pp; English
estrogen receptor-beta protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 90.4%;
Best Local Similarity 99.2%;
Matches 481; Conservative (
                                                                                                                                                                            98WO-US018030.
                                                                                                                                                                                                            97US-00923708
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Webb P;
                                                                                                                                                                                                                                        (REGC ) UNIV CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 485 AA;
                                                                                                                                                                                                              04-SEP-1997;
                                differential
                                                                                Homo sapiens
                                                                                                              W09911760-A1
                                                                                                                                                                            31-AUG-1998;
                                                                                                                                              11-MAR-1999
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Scanlan TS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                           A novel human orphan receptor (AAW14724) is related to the known ocstrogen receptor ER-alpha, and has been designated ER-beta. It is an ocstrogen receptor-related nuclear receptor. The ER-beta amino acid sequence was deduced from a CDNA clone (AAT62843) isolated from a human testis cDNA library. Rat, human and mouse ER-beta (AAW14723-25) can be used to isolate molecules for use in the treatment of cardiovascular diseases, central nervous system diseases, osteoporosis, prostate or ovarian cancer or benign prostatic hyperplasia and to test environmental chemicals for oestrogenic activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAPFTEASWAMSLTKLADKELVHMISWAKKIPQFVELSLPDQVRLLESCWMEVLMMGLMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RSIDHPGKLIFAPDLVLDRDEGKCVEGILBIFDMLLATTSRFRBLKLQHKEYLCVKAMIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INSSMYPEVTATODADSSRKLAHLINAVTDALVWVIAKSGISSOOOSMRLANLLMLISHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LNSSMYPLVTATQDADSSRKLAHLLNAVTDALVWVIAKSGISSQQQSMRLANLLMLLSHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RHASNKGMEHLLINMKCKNVVPVYDLLLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RHASNKGMBHILINMKCKNVVPVYDLILEMLMAHVLRGCKSSITGSECSPAEDSKSKEGSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RSIDHPGKLIFAPDLVLDRDEGKCVEGILEIFDMLLATTSRFRELKLQHKBYLCVKAMIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46 MTFYSPAVMNYSIPSNYTNIEGGPGROTTSPNVLWPTPGHLSPLVVHRQLSHLYAEPQKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PWCEARSLEHTLPVNRETLKRKVSGNRCASPVTGPGSKRDAHPCAVCSDYASGYHYGVWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MTFYSPAVMNYSIPSNVTNLEGGPGRQTTSPNVLWPTPGHLSPLVVHRQLSHLYAEPQKS
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                                                                                                New isolated oestrogen receptor beta - used to develop prods. for treating e.g. cancers, CNS diseases, osteoporosis or cardiovascular
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                                                                                                                                                                                                                                                                                                                                                                                              Length 485;
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                                                                                                                                                                                                                                                                                                                                                                                            Score 2554; DB 2;
Pred. No. 1.9e-234;
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                        Gustafsson
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                                                                                                                                                                   Claim 1; Fig 13A; 45pp; English
                                                                                                                                                                                                                                                                                                                                                                                              Query Match 91.1%;
Best Local Similarity 99.8%;
Matches 484; Conservative
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                      Bnmark E,
                                                       WPI; 1997-192842/17.
N-PSDB; AAT62843.
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                                                                                                                                                                                                                                                                                                                                                                 Sequence 485 AA;
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165 120 225

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465

420 525 480

AAYO1597 ID AAYO XX XX AC AAYO XX XX

345 300 405 360

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This sequence represents a novel oestrogen binding protein. The cDNA sequence which encodes this protein can be alternatively spliced resulting in the detection of additional transcripts (see AAT88413). This receptor is able to bind and be activated by estradiol, estone and estrich, can be used in a screening assay for the identification of new drugs e.g. novel ligands or hormonal analogues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 SADEQLHCAGKAKRSGGHAPRVRELLLDALSPEQLVLTLLEAEPPHVLISRPSADFTEAS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BHTLPVNRETLKRKVSGNRCASPVTGPGSKRDAHFCAVCSDYASGYHYGVMSCBGCKAFF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 MNYSIPSNVTNLEGGPGRQTTSPNVLWPTPGHLSPLVVHRQLSHLYAEPQKSPWCEARSL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 EHTLPVNRETLKRKVSGNRCASPVTGPGSKRDAHFCAVCSDYASGYHYGVWSCEGCKAFP 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KRSIQGHNDYICPATNQCTIDKNRRKSCQACRLRKCYEVGMVKCGSRRBRCGYRLVRRQR 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234 SADEQLHCAGKAKRSGGHAPRVRELLLDALSPEQLVLTLLRAEPPHVLISRPSAPFTRAS 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MNYSIPSNVTNLEGGFGGPTGTTSPNVLMPTFGHLSPLVVHRQLSHLYAEPQKSPWCEARSL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding estrogen receptor - useful in screening assay to identify novel ligands or hormonal analogues.
                                                                                                                                                                                                               Oestrogen receptor protein; steroid; alternative splicing; estradiol;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89.9%; Score 2522; DB 2; L. 100.0%; Pred. No. 2.1e-231; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 18-20; 45pp; English.
                                                                                       AAW33212 standard, protein; 477 AA.
                                                                                                                                                                                 Human oestrogen receptor protein.
                                                                                                                                                                                                                                                                                                                                                97EP-00200903
                                                                                                                                                                                                                                                                                                                                                                               96EP-00200820
                                                                                                                                                                                                                                                                                                                                                                                            96EP-00203284.
                                                                                                                                                                                                                               estone; estriol; screening
                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 477; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mosselman S, Dijkema R;
                                                                                                                                                                                                                                                                                                                                                                                                                         (ALKU ) AKZO NOBEL NV.
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N-PSDB; AAT88412
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                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                   20-APR-1998
                                                                                                                                                                                                                                                                                                                                                25-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                               26-MAR-1996;
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                                                                                                                                                                                                                                                                                    BP798378-A2.
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                                                                                                                      AAW33212;
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        Qy
        354 LIPAPDLVLDRDEGKCVEGILEIPDMLLATTSRFRELKLOHKEYLCVKAMILLANSSMYPL 413

        Db
        301 LIFAPDLVLDRDEGKCVEGILEIPDMLLATTSRFRELKLQHKEYLCVKAMILLNSSMYPL 360

        Qy
        414 VTATQDADSSRKLAHLLANAVTDALVWVIAKSGISSOQOSMRLANLLAHLISHVRHASNKGM 473

        Db
        361 VTATQDADSSRKLAHLLANAVTDALVWVIAKSGISSOQOSMRLANLLAHLISHVRHASNKGM 420

        Qy
        474 EHLLAMKCRAVVPVYDLLLEMLNATURGKKSSITGSSCSPAEDSKSKEGSONPQSQ 530

        Qy
        474 EHLLAMKCRAVVPVYDLLLEMLANATURGCKSSITGSSCSPAEDSKSKEGSONPQSQ 530

        Db
        421 EHLLAMKCRAVVPVYDLLLEMLANATURGCKSSITGSECSPAEDSKSKEGSONPQSQ 530

        Db
        421 EHLLAMKCRAVVPVYDLLLEMLANATURGCKSSITGSECSPAEDSKSKEGSONPQSQ 477
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Search completed: June 20, 2004, 10:37:11 Job time : 62 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

June 20, 2004, 10:35:07; Search time 21 Seconds Run on:

(without alignments)
2427.691 Million cell updates/sec

US-08-906-365-2 2805 Title: Perfect score:

1 MDIKNSPSSLNSPSSYNCSQ......ECSPARDSKSKEGSQNPQSQ 530 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 283366 segs, 96191526 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

χ	Description	TOTAL STATE OF THE				estrogen receptor	$\overline{}$	Н		estrogen receptor	ogen	O		estrogen receptor	steroid hormone re	estrogen receptor	steroid hormone re	retinoid-X-recepto	progesterone recep	progesterone recep	н	retinoic acid rece	retinoid X recepto	glucocorticoid rec	retinoid X recepto	RXR-betal isoform	retinoic acid rece	androgen receptor		retinoic acid rece
SUMMARIES	DI	105929	871400	JW0046	ORCHE	ORHUE	147140	ORMSE	ORRTE	ORXLE	T10423	864737	S58224	A37197	B29345	S58087	A29345	A43781	A39596	153280	A34418	A41651	837781	860586	041727	184718	826669	JG0194	A25923	826670
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	Length	530	477	503	589	595	595	593	600	586	620	701	535	574	433	433	521	467	923	923	446	451	533	758	448	520	410	848	930	463
	ouery Match	100.0	89.9	81.4	43.9	43.7	43.5	43.4	43.4	43.3	42.7	41.9	40.4	39.9	22.5	22.1	21.3	16.8	16.7	16.6	16.4	16.4	16.3	16.3	16.3	16.3	16.2	16.1	16.1	16.1
	Score	2805	2522	2284	230.	1224.5	219.	218.	1216.5	1214	1199	1174.5	1134.5	н	631.5	619.5	597.5	471	469.5	465	459	459	458.5	457.5	456	456	455.5	453	453	452
	Result No.		8	m	Qt	ເກ	w	7	80	σ.	10	FF			14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

retinoid-X recepto	progesterone recep	probable hormone r	mineralocorticoid	retinoid X recepto	retinoid X recepto	retinoic acid rece	probable nuclear h	progesterone recep	glucocorticoid rec	mineralocorticoid	retinoid receptor	nerve growth facto	glucocorticoid rec	retinoid X recepto	androgen receptor
B41727	QRHUP	ORMSN1	A29513	150515	A47278	S26668	A37251	A35466	S44047	A41401	D41977	JQ0623	ORHUGA	509592	A35895
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463	933	601	984	441	467	467	598	786	116	981	470	563	777	462	899
16.1	16.1	16.0	16.0	15.9	15.8	15.8	15.8	15.8	15.7	15.7	15.7	15.7	15.6	15.6	15.6
452 16.1	451 16.1	447.5 16.0	447.5 16.0	446 15.9					441.5 15.7		441 15.7	441 15.7	438.5 15.6		438 15.6

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61 NVTNLEGGPGROTTSPNVLMPTPGFILSPLVVHRQISHLYARPQKSPMCEARSLEHTLPVN 120
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estrogen receptor beta - human
C;Species: Homo sapiens (man)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MDIKNSPSSLNSPSSYNCSQSILPLEHGSIYIPSSYVDSHHEYPAMTFYSPAVNYSIPS
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                                                                                                                                                                                                                                                                                                                                                                                                                   1 MDIKNSPSSLNSPSSYNCSQSILPLEHGSIYIPSSYVDSHHEYPAMTFYSPAVMNYSIPS
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301 LADKELVHMISWAKKIPGFVELSLFDQVRLLESCWMEVLMWGLMWRSIDHPGKLIFAPDL 360

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421 DSSRXLAHILIMAVTDALVWVTAKSGISSQQQSMRLANLLMLLSHVRHASNKGMEHLLIMK 480

361 VLDRDEGKCVEGILEIFDMLLATTSRFRBLKLQHKBYLCVKAMILLNSSMYPLVTATQDA 420

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C, Date: 17-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 17-Mar-1999
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A; Residues: 1-589 < MAX>
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C; Reywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone recepts; 94-35; Domain: erbA transforming protein homology CRRA>
F; 94-35; Domain: erbA transforming protein homology CRRA>
F; 96-116; Region: zinc finger CCCC motif
F; 96-116; Region: zinc finger CCCC motif
F; 96-128; Region: nuclear location signal
F; 52; Sinding site: phosphate (Ser) (covalent) (by MAP kinase) #status predicted
F; 96, 99; 113, 116; Binding site: zinc (Cys) #status predicted
F; 132, 138, 148, 151; Binding site: zinc (Cys) #status predicted
                                                                                                                                                                                                                                                 C;Accession: S71400 T: Dijkema, R. R:Mosselman, S:; Polman, J:; Dijkema, R. FEBS Lett. 392, 49-53, 1996 A;Title: BR-beta: identification and characterization of a novel human estrogen receptor A;Reference number: S71400; MUID:96354875; PMID:8769313 A;Accession: S71400
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DSSRKLAHLINAVTDALVWVIAKSGISSQQQSMRLANLIMLLSHVRHASNKGMEHLLNMK 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 MNYSIPSNVTNLEGGPGRQTTSPNVLWPTPGHLSPLVVHRQLSHLYAEPQKSPWCEARSL 113
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                                                                                                                                                                                                               Species: Homo sapiens (man)
|Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 20-Jun-2000
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                                                               CKNVVPVYDLILLEMINAHVIRGCKSSITGSECSPAEDSKSKEGSQNPQSQ 530
                                         CKNVVPVYDLILEMIANAHVIRGCKSSITGSECSPAEDSKSKEGSQNPQSQ 530
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                                                                                                                                                                                           estrogen receptor beta - human
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A;Residues: 1-477 <MOS>
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estrogen receptor beta2 - rat N;Alternate names: ERbeta2 C;Species: Rattus norvegicus (Norway rat)

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C)Accession: UN0046
R;Maruyama, K.; Endoh, H.; Sasaki-Iwaoka, H.; Kanou, H.; Shimaya, E.; Hashimoto, S.; K;
Biochem. Biophys. Res. Commun. 246, 142-147, 1998
A;Title: A novel isoform of rat estrogen receptor beta with 18 amino acid insertion in A;Reference number: UW0046; MUID: 98262932; PMID: 9600083
A;Accession: UW0046
A;Molecule type: mRWA
A;Residues: 1-503 «MAR»
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C;Species: Gallus gallus (chtcken)
C;Date: 06-Mar-1992 #sequence_revision 14-Jul-1994 #text_change 22-Jun-1999
C;Datession, A40914; S07192
R;Maxwell, B.L.; McDonnell, D.F.; Conneely, O.M.; Schulz, T.Z.; Greene, G.L.; O'Malley, Mol. Endocrinol. 1, 25-35, 1987
Mylles: Structural organization and regulation of the chicken estrogen receptor. A;Reference number: A40914, MUID:88318621; PMID:2901032
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A.Title: The chicken cestrogen receptor sequence: homology with v-erbA and the human of A.Reference number: S07192; MID:86247578; PMID:3755102
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C;Comment: This protein functions as a negative regulator of estrogen action.
C;Superfamily: estrogen receptor; erbA transforming protein homology
F;102-381/Domain: erbA transforming protein homology <ERBA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46 MTFYSPAVMNYSIPSNVTNLEGGPGRQTTSPNVLWPTPGHLSPLVVHRQLSHLYAEPQKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166 CEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLRKCYEVGMVKCGSRRBRCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               388 RELKLOHKEYLCVKAMILLNSSMYPLVTATODADSSRKLAHLLNAVTDALVWVIAKSGIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    448 SQQQSMRLANLLMLLSHVRHASNKGMEHLLNMKCKNVVPVYDLLLEMLNAHVLRGCKSSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YRLVRRORSADEQLHCAGKAKRSGGHAPRVRBLLLDALSPEQLVLTLLEAEPPHVLISRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 81.4%; Score 2284; DB 2; Length 5 Best Local Similarity 85.9%; Pred. No. 2.9e-170; Matches 432; Conservative 23; Mismatches 30; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 508 TGSECSPAEDSKSKEGSONPOSO 530
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A,Accession: A94284
A,Molecule type: mRNA
A,Rocession: A94284
A,Molecule type: mRNA
A,Rocession: A94286
A,Molecule type: mRNA
A,Rocession: S: Walter, P.; Kumar, V.; Krust, A.; Bornert, J.M.; Argos, P.; Chambon, P.
R,Green, S: Walter, P.; Kumar, V.; Krust, A.; Bornert, J.M.; Argos, P.; Chambon, P.
R,Green, S: Walter, P.; Kumar, V.; Krust, A.; Bornert, J.M.; Argos, P.; Chambon, P.
A,Rocession: A93376, MUID:86146892; PMID:3754034
A,Rocession: A93376
A,Molecule type: mRNA
A,Residues: 1595 <GR2
A,Rocession: A93376
A,Molecule type: MNA
A,Reference mumber: A93021, MUID:89091079; PMID:3145193
A,Rocession: A43021
A,Molecule type: DNA
A,Reference number: A43021; MUID:89091079; PMID:3145193
A,Rocession: A43021
A,Molecule type: DNA
A,Reference number: A93021, MUID:9091079; PMID:3145193
A,Reference number: A93021
A,Reference analysis of the S' flanking region of the human estrogen receptor ger
A,Reference number: S27140; MUID:93075998; PMID:1476547
A,Reference number: S27140; MUID:93075998; PMID:1476547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Reterence number: S14000, MUID:93153765, FWID:7916651
A, Reterence number: S14000, MUID:93153765, FWID:7916651
A, Accession: S14000
A, Status: Preliminary
A, Modecule type: mRNA
A, Residues: 216.754, 367.399, GC, 401-434 cPFB
A, Crose references: BMGL:473067; MUD:9579865; PIDN:CA551528.1; PID:9939886
A, Crose references: BMGL:473067; MUD:9579865; PRD:CA50164 to authbris translated the codon GGG for residue 400 as Val
R, Mocresion: A1922
A, Filtie: Glaracterization of estrogen receptor variant mRNAs from human breast cancers.
A, Reference number: A41925, MUD:9229154; PMID:1920386
A, Rocession: A41925
A, Modecule type: mRNA
A, Residues: 1.244 'Elbrack coorder
A, Noce: sequence extracted from NCBI backbone (NCBIN:106580)
A, Rocession: BH:08297; MUD:0918218; PIDN:AAA58462.1; PID:9182219
A, Rocession: BH:08297; MUD:0918218; PIDN:AAA58462.1; PID:9182219
A, Rocession: BH:08297; MUD:09182218; PIDN:AAA58462.1; PID:9182219
A, Noce: sequence extracted from NCBI backbone (NCBIN:106580)
A, Noce: sequence extracted from NCBI backbone (NCBIN:106580)
A, Rocession: BH:0829
A, Roce
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A;Molecule type: DNA
A;Cross-references: EMBL:X62462; NID:g31201; PIDN:CAA44322.1; PID:g31205
B;Pfeffer, U.; Pecarotta, E.; Castagnetta, L.; Vidali, G.
Cancer Res. 53, 741-743, 1993
A;Title: Betrogen receptor variant messenger RNA lacking exon 4 in estrogen-responsive
A;Reference number: S34000; MUID:93153765; PMID:7916651
Rigreene, G.L.; Gilna, P.; Waterfield, M.; Baker, A.; Hort, Science 231, 1150-1154, 1986
A; Title: Sequence and expression of human estrogen receptor A; Reference number: A94284; WUID:86122927; PMID:3753802
    A;Status; preliminary
A;Status; preliminary
A;Status; preliminary
A;Molecule type: mRNA
A;Essidues: 1.256, "B',258-589 <KRU>
A;Molecule type: mRNA
A;Residues: 1.256, "B',258-589 <KRU>
A;Actions=references: Embi.KX03005; NID:G33378; PIDN:CAA27433.1; PID:g63380
C;Comment: The steroid hormones and their receptors are involved in the regulation of events: The steroid hormone receptors are thought to be weakly
C;Comment: The steroid hormones and their receptors are involved in the regulation of events: appears to recognize discrete DNA sequences upstream of transcriptional start sit
C;Superfamily: estrogen receptor; erbA transforming protein homology
C;Reywords: DNA binding; nucleus; phosphorotein; steroid binding; steroid hormone receptor; erbA transforming protein homology <C;Reywords: DNA binding #status predicted <DNA>
F;177-450/Domain: DNA binding #status predicted <DNA>
F;177-450/Domain: erbA transforming protein homology <ERBA>
F;177-450/Domain: crbA transforming protein homology <ERBA>
F;177-450/Momain: erbA transforming site: zinc (Cys) #status predicted
F;215,221,231,234/Binding site: zinc (Cys) #status predicted
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N;Alternate names: ER1; estrogen receptor alpha
C;Species: Homo sapiens (man)
C;Date: 28-May-1986 #sequence revision 28-May-1986 #text change 22-Jun-1999
C;Accession: A94284; A93376; Ā43021; S27143; S34000; A41525; B41925; A03244; C41925; l
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161 STNEKGSLSMESTK-ETRYCAVCNDYASGYHYGVWSCEGCKAFFKRSIQGHNDYMCPATN 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 220 QCTIDKNRRKSCQACRIRKCYEVGWAKGGIRKDRRGGRWYKQKRQREEQDSRNGEASSTE 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QCTIDKNRRKSCOACRLRKCYEVGNVKCGSRRERCGYRLVRRORSADEQLHCAGKAKRSG
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43.9%; Score 1230.5; DB 1; Length
Best Local Similarity 47.3%; Pred. No. 5.2e-88;
Matches 259; Conservative 93; Mismatches 126; Indels
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KEEESMQN 587
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D41

complementary

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A; Experimental source: uterus
R; Thole, H.H.
FEBS Lett. 320, 92-96, 1993
A; Title: Assignment of the ligand binding site of the porcine estradiol receptor to the A; Reference number: S32402; MUID:93209384; PMID:8458437
A; Reference number: S32402; MUID:93209384; PMID:8458437
A; Recession: S32402
A; Residues: 309-323 < THW>
C; Reywords: 100-323 < THW>
C; Reywords: 100-323 < THW>
C; Reywords: DNA binding; nucleus; phosphoprotein; steroid hormone receptor; transcript: C; Reywords: DNA binding; nucleus; predicted < DNA>
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F; 121-299/Domain: erbA transforming protein homology < ERBA>
F; 185-205/Region: zinc finger CCCC motif F; 221-245/Region: zinc finger CCCC motif F; 255-271/Region: muclear location signal F; 300-595/Domain: steroid binding #status predicted
F; 221, 227, 237, 240/Binding site: zinc (Cys) #status predicted
F; 236, 305/Binding site: zinc (Cys) #status predicted
F; 237, 237, 240/Binding site: zinc (Cys) #status predicted
F; 237, 237, 240/Binding site: zinc (Cys) #status predicted
F; 237, 237, 240/Binding site: zinc (Cys) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302 ADKELVHMISWAKKIPGEVELSLFDQVRLLESCWMEVLAMGLMWRSIDHPGKLIFAPDLV 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  estrogen receptor - mouse
C;Species: Mus musculus (house mouse)
C;Dacies: 06-Mar-1992 #sequence_revision 14-Jul-1994 #text_change 22-Jun-1999
C;Accession: A40061
R;White, R.; Lees, J.A.; Needham, M.; Ham, J.; Parker, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Length 595;
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43.5%; Score 1219.5; DB 2; Length
Best Local Similarity 46.0%; Pred. Mo. 3.8e-87;
Matches 268; Conservative 89; Mismatches 126; Indels
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cispecies: Sus scrofa domestica (domestic pig)
Cispecies: Sub-cispecial (domestic pig)
Cispecies: Sub-cispecial (domestic pig)
Cispecies: Sub-cispecial (domestic pig)
Mol. Cell. Endocrinol. 104, 163-172, 1994
A.Title: The C-terminal half of the porcine estradiol receptor contains no post-A; Reference number: 147140; MUID:95080454; PMID:7983744
A.Title: The C-terminal half of the MID:95080454; PMID:788764
A; Residues: 1-595 - ROM:
A; Residues: 1-595 - ROM:
A; Residues: Describer: Sub-cispecial (domestic pig)
A; Ribole H.H.; Maschler, 1:; Mungblut, P.W.
Eur: J. Biochem 211, 510-516, 1995
A; Title: Surface mapping of the ligand-filled C-terminal half of the porcine est A; Reference number: S66250; MUID:95361877; PMID:7635163
A; Molecule type: protein
A; Residues: 297-307;310-313;320-323;337-340;417-420;466-473 <THO>
A; Residues: 297-307;310-313;320-323;337-340;417-420;466-473 <THO>
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                                                                                                                                                                                                                                                                                                75 Q-TGLPYGPGSEAAAFGSNGLGGFPPLNSVSPSPLMLLHPPPQLSPFLQPHGQQVPYYLB
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                                                                                                                                                                                                                                                                        ---TISPNVLWPTPGHLSP-LVVHRQLSHLYAE
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    P;185-205/Region: zinc finger CCCC motif
P;221-245/Region: zinc finger CCCC motif
P;230-595/Domain: stercold binding #sterus predicted <STB>
P;236,305/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                                                63
                                                                                                      Query Match
43.7%; Score 1224.5; DB 1; Length
Best Local Similarity 48.3%; Pred. No. 1.6e-87;
Matches 263; Conservative 88; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215 VKCGSRRERCGYRLVRRQRSADEQLHCAGKAKRSGGHAPRVR----
                                                                                                                                                                                                                                                                          61 NVTNLEGGPGRQ-----
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C; Accession: S07379; S16731

R; Koike, S.; Sakai, M.; Murzanteu, M.

Nucleic Acids Res. 15, 2499-2513, 1987

Nucleic Acids Res. 15, 2499-2513, 1987

A; Title: Wolecular cloning and characterization of rat estrogen receptor CDNA.

A; Rice and the control of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 NELEPLINRP-----QLKMFMERALGEVYVDNS-KPAVFNYPEGAAYEFNAAAAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 CRIRKCYEVGWVKCGSRRERCGYRLVRRQRSADB----QLHCAGKAKRSG-----G
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     Mol. Endocrinol. 1, 735-744, 1987

A,Title: Structural organization and expression of the mouse estrogen receptor.

A,Rccession. A40061

A,Accession. A40061

A,Cross-references. GB:M38651; NID:g193179; PIDN:AAA37580.1; PID:g193180

C,Comment. The steroid hormones and their receptors are involved in the regulation of eu C,Comment. The steroid hormone receptors are thought to be weakly omplex appears to recognize discrete DNA sequences upstream of transcriptional start sit C,Comment. In the absence of ligand, steroid hormone receptors are thought to be weakly omplex appears to recognize discrete DNA sequences upstream of transcriptional start sit C,Superfamily: estrogen receptor; phosphoprotein, steroid binding; steroid hormone receptors are by binding flattue predicted <DNA.

F,187-420/Domain: DNA binding flattue predicted <DNA.

F,187-420/Domain: erbA transforming protein homology <ERBA.

F,187-420/Domain: erbA transforming predicted <STB.

F,304-556/Domain: steroid binding flattus predicted <STB.

F,189-120,209/Binding site: zinc (Cy8) #status predicted
F,220,309/Binding site: zinc (Cy8) #status predicted
F,220,309/Binding site: zinc (Cy8) #status predicted
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311 AL--SLTADQMVSALEDABPPMIYSEYDPSRPFSBASWMGLLTMLADRELVHMINWAKRV 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YAEPQKSPWCEARSLEHTLP---VNRETLKRKVSGNRCASPVTGPG----SKRDAHFCA 150
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estrogen receptor - rat
C.Species: Rattus norvegicus (Norway rat)
C.Spate: 30-Sep-1991 #sequence_revision 14-Jul-1994 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VCSDYASGYHYGVWSCEGCKAPFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLRKCY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.4%; Score 1218.5; DB 1; Length
45.8%; Pred. No. 4.6e-87;
live 98; Mismatches 152; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAHVLRGCKSSITGSECSPAEDSKSKEGSQNPQS 529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 EQLHCAGKAKRS--GGHAPRVRELLLDALSPEQLVLTLLEAEPPHVLISRP--SAPFTEA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 345 TWWTILTSMADKELVHMIAWAKKLPGFLQLSLHDQVLLLESSWLBVLMIGLIWRSIHCPG 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              293 SMMMSLITKLADKELVHMISWAKKIPGPVELSLFDQVRLLESCWMEVLMMGLMWRSIDHPG 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLIFAPDLVLDRDEGKCVEGILEIFDMLATTSRFRELKLQHKEYLCVKAMILLNSSMYP 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80
                                                                                                                 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTPGHLSPLVVHRQLSHLYABPQKSPWCEARSLEHTLPVNRETLKRKVSGNR----CASPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 TGPGS-----KRDAHFCAVÇSDYAŞGYHYGYWSÇEGCKAFFKRSIQGHNDYIÇPATNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 YVDSHHEY----PAMT-----FYSPAVMNYSIPS--NVTNLEGGPGRQTTSPNVLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              413 IVTATOD-ADSSRKLAHLLNAVTDALVWVIAKSGISSOOOSMRLANLLMLLSHVRHASNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 465 FCTGTMEPLHNSAAVQSMLDTITDALIHYISQSGYLAQEQARRQAQLLLLLSHIRHMSNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GWEHLYSMKCKNKVPLYDLILEMLDAHRLHHPVRAPQSLSQVDRDPPSTSSGGGGIAPGS
                                                                                                                                                                                                                                                                                                                               AjGene: MER
(Superfamily: estrogen receptor; erbA transforming protein homology
CjKeywords: DNA binding; nucleus; steroid hormone receptor; transcription
P;184-460/Domain: erbA transforming protein homology <ERB>
                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
                                                                                                                                                                                                                                                                                                                                                                                                                Length 620;
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
42.7%; Score 1199; DB 2; Length 6
Best Local Similarity 48.1%; Pred. No. 1.6e-85;
Matches 265; Conservative 81; Mismatches 129; Indels
                                                                         C.Species Coryalas sp. Natrain G-IK)
C.Species Coryalas sp. Natiety: Strain d-IR
A;Variety: Strain d-IR
C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_ch
C;Accession: Ti0423
R;Okada, H.; Kawahara, T.; Yamashita, I.
A;Bescription: Cloning of medaka estrogen receptor CDNA.
A;Reference number: Zi7013
A;Reference number: Zi7013
A;Residues: 1-620 <OKA>
A;Residues: 1-620 <OKA>
A;Residues: I-620 <OKA>
A;Residues: GMBL:D28954
C;Genetics:
                                                                  d-rR)
                                                                    (strain

    Oryzias sp.

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S64737
80K estrogen receptor - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 222 CTIDKNRRKSCQACRLRKCYEVGAMKGGIRKDRRGGRLLKHKRQKEEQ----EQKNDVD 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 337 LLTNLADRELVEMINWAKRVPGFVDLTLHDQVHLLECAWLSILAYGLIWRSVEHPGKUSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 YVDSHH----EYP-----AMTFYSPAVMNYSIPSNVTNLEGGPGRQT----TSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 NVIMPTPGHISPLAVHR-QUSHLYARPQKSPWCBARSLEHTLPVARBTLKRKVSGARCAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 VVFLAKLPQLSPFIHHHGQQVPYYLESEQGTFAVREAAPPTF-YRSSEDNRRQSGRERMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTIDKNRRKSCQACRLRKCYEVGMVKCGSRRBRCGYRLVRRQRSADEQLHCAGKAKRSGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 43.3%; Score 1214; DB 1; Length 586; Il Similarity 48.6%; Pred. No. 1e-86; 255; Conservative 82; Mismatches 138; Indels 5:
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Best Local S
Matches 255
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242 LFLLQGAEPP-ALCSROKVARPYTEVTWYTLLTSWADKELVHWIAWAKKVPGPQELSLHD 300
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C;Species: Oncorpyrathus writes (rainbow trout)
C;Date: 31-3n-1992 #sequence_revision 31-Jan-1992 #text_change 20-Aug-1999
C;Accession: A37197; A40070
R;Pakdel, F.; Le Gac, F.; Le Goff, P.; Valotaire, Y.
Mol. Cell. Endocrinol. 71, 195-204, 1990
A;Title: Full-length sequence and in vitro expression of rainbow trout estrogy A;Reference number: A37197; MuID: 91006824; PMID: 2210031
A;Accession: A37197
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-574 cPRK>
A;Cross-references: GB:N31559
A;Cross-references: GB:N31559
A;Cross-references: GB:N31559
A;Title: Identification and estrogen induction of two estrogen receptors (ER)
A;Reference number: A40070; MUID: 8917284; PMID: 2915648
      R;Rogers, S.A.; Llewellyn, L.; Ramsurn, V.P.; Sweeney, G.E.; Wigham, T. submitted to the EMBL Data Library, July 1995
A;Reference number: SS8224
A;Accession: SS8224
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-535 < ROG>
A;Cross-references: EMBL:X88959; NID:9929901; PIDN:CAA61999.1; PID:9929902
C;Superfamily: estrogen receptor; erbA transforming protein homology
C;Keywords: steroid hormone receptor; zinc finger
F;103-382/Domain: erbA transforming protein homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ::| || :: : || |:
188 KRYCGPAGDREKPYGDLEHRTAPPQDGGRNSSSSSLSGGGGWCGPRI-----TMPPEQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 GROTTSPNVLWPTPGHLSPLVVHRQLSH-----LYAEPOKSPWCEARSLEHTLPVNRET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSSPTGPLVFVSSSPQLSPF-LHPPGHHGLPSQSYYLETSSTPLYRSSVVTNQLSASEE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRELKLOHKEYLCVKAMILLNSSMYPLVT-ATODADSSRKLAHLLNAVTDALVWVIAKSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----SPGKVAQAGEQTEGPST 493
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C;Species: Homo sapiens (man)
C;Species: Bocc-1996 #sequence_revision 13-Mar-1997 #text_change 20-Aug-1999
C;Date: 28-Occ-1996 #sequence_revision 13-Mar-1997 #text_change 20-Aug-1999
C;Accession: S6473.
Wu, S.Q.; Wolf, D.M.; Bilimoria, M.M.; Jordan, V.C.
Nucleic Acids Res. 24, 962-969, 1996
A;Title: A novel 80 kDa human estrogen receptor containing a duplication of exons 6 and A;Reference number: S64737; MUID:96174665; PMID:8600466
A;Accession: S64737
A;Scatus: preliminary; nucleic acid sequence not shown; translation not shown A;Residues: 1-701 cPIN.
A;Residues: 1-701 cPIN.
A;Residues: 1-701 cPIN.
A;Residues: 1-701 cPIN.
A;Cross-references: EMB:.U47678; NID:91197864; PIDN:AAB00115.1; PID:91197855
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1996
C;Superfamily: estrogen receptor; erbA transforming protein homology
C;Keywords: steroid hormone receptor; zinc finger
F;183-456/Domain: erbA transforming protein homology #status atypical cERB2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41.9%; Score 1174.5; DB 2; Length 701; llarity 41.2%; Pred. No. 1.5e-83; Conservative 87; Mismatches 125; Indels 171;
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Oestrogen receptor - Atlantic salmon (fragment)

O'Species: Salmo salar (Atlantic salmon)

C;Date: 13-Jan.1996 #sequence_revision 01-Mar-1996

C;Accession: $58224
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Best Local Similarity
Matches 268; Conservat
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241 326

123

71; 535;

2; Length

74

177 133 237 445 420

360

476

rainbow trout estrogen recepto

20-Aug-1999

(ER) messenger

#text_change 20-Aug-1999

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142;
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N
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 150-574 < PA2>
A;Residues: 150-574 < PA2>
A;Residues: 150-574 < PA2>
A;Cross-references: GB:M31559; NID;g213783; PIDN:AAA49552.1; PID:g213784
A;Cross-references: GB:M31559; NID;g213783; PIDN:AAA49552.1; PID:g213784
C;Superfamily: estrogen receptor; erbA transforming protein homology
C;Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation; P;147-167/Region: zinc finger
P;183-207/Region: zinc finger
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                                                                                                                                                                70 GRQTTSPNVLWPTPGHLSPLV---VHRQLSH-----LYAEPOKSPWCEARSLEHTLPVN
                                                                                                                                          58;
                                                                                                                    Length 574;
                                                                                                                    Query Match 39.9%; Score 1120; DB 2; Length 5 Best Local Similarity 48.8%; Pred. No. 2.1e-79; Matches 243; Conservative 70; Mismatches 127; Indels
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103 209 163 263 217 268 ä 셤 ò 셤 ठे 성 음 장 Š staroid hormone receptor ERR2 precursor - human
C.Species: Howo sapiens (man)
C.Species: Howo sapiens (man)
C.Species: Howo sapiens (man)
C.Accession: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 20-Sep-1999
C.Accession: 1829345
B.Giguere, V.; Yang, N.; Segui, P.; Evans, R.M.
Nature 31, 91-94, 1988
A.Title: Identification of a new class of steroid hormone receptors.
A.Reference number: A29345
A.MID:88122546; PMID:3267207
A.Residues: 1-433 <GIG-A.Residues: 1-433 <GIG-

Score 631.5; DB 2; Length 433; Pred. No. 1.8e-41;

22.5%; 39.3%;

Query Match Best Local Similarity

estrogen receptor related protein - mouse (Species: Mus musculus (house mouse) (Spaces: Mus musculus (house mouse) (Spaces: Mus musculus (Spaces: Musculu homology 10, 216 323 SLFDQVRLLESCWMEVLMWGLMWRSIDHPGKLIFAPDLVLDRDEGKCVEGILEIFDWALLA 382 162 205 320 265 380 324 438 162 262 322 267 266 A,Cross-references: EMBL:X89594; NID:g914855; PIDN:CAA61755.1; PID:g914856 C;Superfamily: unassigned erbA-related proteins; erbA transforming protein C;Keywords: steroid hormone receptor; zinc finger F;101-352/Domain: erbA transforming protein homology <BRBA> 267 QLVLT-----LLEAEPPHVLISRP-SAPFTEASMAMSLTKLADKELVHMISWAKKIPGFV 321 ELSLFDOVRLLESCHMEVLAMGLAMRSIDHPGKLIFAPDLVLDRDEGKCVEGILEIFDML LATTSRFRELKLOHKEYLCVKAMILLNS-SNYPLVTATODADSSRKLAHLLN-AVTDALV LQLVRRYKKIKVEKEBFVWIKALALANSDSMY----IENLEAVQKLQDLIHSALQDYEL WVIAKSGISSQQQSMRLANLLMLLSHVRHASNKGMEHLLNMKCKNVVPVYDLLLBMLNAH CYEVGMVKCGSR--RERCGYRLVRRORSADE----QLHCAGKAKRSGGHAPRVRELLLDA TISRERELKI, OHKEYL CVKAMILLINS - SMYPLVTATQDADSSRKI, AHLLIN - AVTDALVWV SORHEEPRRAGKLILTLPILRQTAAKAVQHFYSVKLQGKVPMHKLFLEMLRAK 149 CAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLRK LSPEQLVLTLLEAEPPHVLISRPSAPFTEASMMMSLTKLADKELVHMISWAKKIPGFVBL CYEVGMVKCGSR--RERCGYRLVRRORSADBOLHCAGKAKRSGGHAPRVRELLLDALSPE 149 CAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLRK 36; Gaps Gaps 40; 433; Length Indels Query Match 22.1%; Score 619.5; DB 2; Best Local Similarity 38.7%; Pred. No. 1.6e-40; Matches 139; Conservative 76; Mismatches 108; Mismatches 69 Conservative 499 V 499 V 433 383 327 ਨੇ D. us-08-906-365-2.rpr

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Search completed: June 20, 2004, 10:39:11 Job time: 22 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

June 20, 2004, 10:31:17; Search time 17 Seconds (without alignments) 1623.364 Million cell updates/sec Run on:

Title:
Perfect score: 3

US-08-906-365-2 2805 1 MDIKNSPSSINSPSSYNCSQ......ECSPAEDSKSKEGSQNPQSQ 530

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 seqs, 52070155 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score	% Query Match	Length	DB	OMPHALISO	Description
2805	1	530	3 -	ESR2 HUMAN	092731 homo sapien
	93.		-	ESR2_CALJA	calli
2496		530	Н	ESR2 RAT	ratt
4 2495		m	-	ESR2 MOUSE	008537 mus musculu
	87.	527	7	ESR2_BOVIN	bos t
	87.	527	7	ESR2_SHEEP	ovis
	86.	526	Н	ESR2_PIG	Q9xsw2 sus scrofa
2101		554	Н	ESR2_STUVU	
9 1959	. 69	472	-	ESR2_COLUA	coturn
7	69	472	Н	BSR2 CHICK	Q9ptu5 gallus gall
	55.	573	Н	ESR2_ANGJA	anguil
	52.	568	Н	SRB1 CARAU	Q9w669 carassius a
13 1440.5	51.	568	П	ESR2 ONCMY	_
		673	-	ESR2_MICUN	micropo
	49.	279	Н	BSR2 MACMU	macaca
1385.5	49.	559	٦	ESR2_SPAU	
1381		575	Н	ESR2_ICTPU	
1378.5	49.	610	-	ERB2_CARAU	_
1373	48	565	Н	ESR3 MICUN	_
1352	48	557	Н	ESR2 ORENI	Q9yh32 oreochromis
4		595	Н	ESR1 HUMAN	
	43	587	н	ESR1 POEGU	
	43	589	Н	ESR1_CHICK	gallus
24 1220	শ	594	-	ESR1 HORSE	Q9tv98 equus cabal
	43	595	-	ESR1 PIG	Q29040 sus scrofa
	43	595	-	ESR1 MESAU	Q9qzj5 mesocricetu
12	43.	59	Н	ESR1 MOUSE	_
1216.	43.4	009	-	ESR1_RAT	
	43	585	-	ESR1 ORENI	Q9yh33 oreochromis
	43.	586	Н	ESR1_XBNLA	٠,
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2 1204	4	579	Н	ESR1_SPAAU	
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042132 pagrus majo P50240 orecchromis P50240 orecchromis P5042 and orecchromen Q9yhz7 ictalurus p P50242 and orec Q9yht3 anolis caro O75454 homo sapien P11475 rattus norv O95718 homo sapien Q61539 mus musculu
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1194.5 1184.5 1177 1165.5 1134.5 1134.5 799.5 631.6 631.5
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## ALIGNMENTS

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unclear vo.;

"CIA, a novel estrogen receptor coactivator with a bifunctional
"CIA, a novel strogen receptor coactivator with a bifunctional
"CIA, a novel strogen interacting determinant.",
"Mol. Cell. Biol. 21:443-353 (2001).

"I Mol. Cell. Biol. 21:443-353 (2001).

"I FUNCTION: Nuclear hormone receptor. Binds estrogens with an affinity similar to that of ESRI, and activates expression of reporter genes containing estrogen response elements (ESE) in an estrogen-dependent manner. Isoform beta-ox lacks ligand binding ability and has no ro nny very low ere binding activity resulting in the loss of ligand-dependent transactivation ability. DNA-binding by ESRI and ESR2 is rapidly lost at 37 degrees Celsius in the absence of ligand while in the presence of 17 beta-estradiol temperature is more gradual.

"SIBUNIT: Binds DNA as a honding at elevated temperature is more gradual.

"SISRI rather than ESR2 and inhibits of bims a heterodimer with ESRI rather than ESR2 and inhibits DNA-binding by ESRI. Interacts with ESRI rather than ESR2 and inhibits DNA-binding by ESRI. Interacts in increase of transcription of target genes.

"Interact ESRILLAR LOCATION: Nuclear.

"Interact ESPERTALILAR LOCATION: Nuclear.

"Interact ESPERTALILAR LOCATION: Nuclear.

"Interact ESPERTALILAR LOCATION: Nuclear.

"Interact ESPERTALILAR ESPERTALICE PRODUCTS:

"ENTIRERNATIVE PRODUCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERACTION WITH MCOA3.
MEDLINE=97410321; PubMed=9267036;
Chen H., Lin R.J., Schiltz R.L., Chakravarti D., Nash A., Nagy L.,
Privalsky M.L., Nakatani Y., Evans R.M.;
"Nuclear receptor coactivator ACTR is a novel histone
acetyltransferase and forms a multimeric activation complex with P/CAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-20148724; PubMed-10681503;
Caira F., Antonson P., Pelto-Huikko M., Treuter E., Gustafsson J.-A.;
"Cloning and characterization of RAP250, a nuclear receptor
                     MEDLINE=98348389; PubMed=9685228;
Lu B., Leygue B., Dotzlaw H., Murphy L.J., Murphy L.C., Watson P.H.;
"Estrogen receptor-beta mENA variants in human and murine tissues.";
Mol. Cell. Endocrinol, 138:199-203(1998).
                                                                                                                                                                                                                                                                                                                                                         Pace P., Taylor J., Suntharalingam S., Coombes R.C., Ali S.; fuluman estrogen receptor beta binds DNA in a manner similar to and dimerizes with estrogen receptor alpha."; J. Biol. Chem. 272:25832-25838(1997).
                                                                                                                                                                               Li L.C., Dahiya R.; "Cloning and characterization of the estrogen receptor beta gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERACTION WITH NCOAS.
MEDLINE-20565767; PubMed=11113208;
Sauve F., McBroom L.D.B., Gallant J., Moraitis A.N., Labrie F.,
Giguere V.,
                                                                                                                                                                                                                                                      Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSP 003686;
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IsoId=092731-3; Sequence=VSP_003684,
Name=4; Synonyms=Beta-3;
IsoId=092731-4; Sequence=VSP_003690;
Name=5; Synonyms=Beta-4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=1; Synonyms=Beta-1;
Isode-092711-1; Sequence=Displayed;
Name=2; Synonyms=Beta-2, CX;
IsoId=092731-2; Sequence=VSP_003689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=292731-5; Sequence=VSP_003691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=6; Synonyms=Beta-5;
IsoId=092731-6; Sequence=VSP_003692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol. Chem. 275:5308-5317(2000).
                                                                                                                                                                                                                                                                                                             CHARACTERIZATION.
MEDLINE=97467383; PubMed=9325313;
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                                                                                                                                                      SEQUENCE OF 1-69 FROM N.A.
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  TISSUE=Ovary
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                         Name=8; Synonyme=Beta-6;

Isola=092731-8; Sequence-VSP 003687, VSP 003688;

Isola=092731-8; Sequence-VSP 003687, VSP 003688;

ovary, and at a lower level in heart, brain, placenta, liver, skeletal muscle, spleen, thymus, prostate, colon, bone marrow, mammary gland and uterrus. Also found in uterine bone, breast, and covarian tumor cell lines, but not in colon and liver tumors. Isoform beta-2 is expressed in spleen, thymus, testis and ovary and at a lower level in skeletal muscle, prostate, colon, small intestine, leukocytes, bone marrow, mammary gland and uterus. Isoform beta-4 is expressed in testis, isoform beta-4 is expressed in testis, and at a lower level in spleen, thymus, ovary, mammary gland and uterus. Isoform beta-5 is expressed in testis, placenta, skeletal muscle, spleen and leukocytes, and at a lower level in heart, lung, liver, kidney, pancreas, thymus, prostate, lower level in heart, lung, liver, kidney, pancreas, thymus, prostate, Not expressed in brain.

c. --- DOMAIN Composed of three domains: a modulating N-terminal domain, a DNA-binding domain and a C-terminal steroid-binding domain.

c. --- SIMILABITY: Belongs to the nuclear hormone receptor family. NR3
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R GO; GO:0005634; C:nucleus; TAS.
R GO; GO:0005634; C:nucleus; TAS.
R GO; GO:0005634; F:setrogen receptor activity; TAS.
R GO; GO:0005496; F:sterofor antagonist activity; TAS.
GO; GO:0003713; F:transcription co-activator activity; TAS.
R GO; GO:0007267; P:call-cell signaling; TAS.
R GO; GO:0007267; P:cell-cell signaling; TAS.
R GO; GO:0007267; P:cell-cell signaling; TAS.
R GO; GO:0007267; P:segulation of cell growth; NAS.
R GO; GO:0007165; P:signal transduction; TAS.
R GO; GO:0007165; P:signal transduction; TAS.
R InterPro; IPR001364; Hormone_receptor.
R InterPro; IPR001364; Str_ncl_receptor.
R InterPro; IPR001464; Str_ncl_receptor.
R Pfam; PF001104; hormone_rec; 1.
IsoId=Q92731-7; Sequence=VSP_003685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB006599; BAA24953.1; EMBL; AP051427; AAC05985.1; EMBL; AP051428; AAC05781.1; EMBL; AP061049; AAC39784.1; EMBL; AP061055; AAC39785.1; EMBL; AP061055; AAC39785.1; EMBL; X99101; CAA67555.1; ALT INIT. EMBL; AP074599; AAC25602.1; EMBL; AP074599; AAC25602.1; EMBL; AP047463; AAC03786.1; EMBL; AP047463; AAC03786.1; EMBL; AP191544; AAP24232.1; ...
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TRANSPAC; T04651; --
TRANSPAC; T05387; --
TRANSPAC; T05389; --
TRANSPAC; T05389; --
TRANSPAC; T05399; --
TRANSPAC; T05391; --
TRANSPAC; T05391; --
Genew; HGNC:3468; ESR2.
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1NDE; 18-DEC-02.
1QKM; 28-JUL-00.
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DOMAIN: Composed of three domains: a modulating N-terminal domain, a DNA-binding domain and a C-terminal steroid-binding domain.
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                                                                                                                                                                                                                                                                                                                                                                    CAGKAKRSGGHAPRVRELLIDALSPEQLVLTILEAEPPHVLISRPSAPFTRASMMSLTR
                                                                                                    MDIKNSPSSINSPSSYNCSQSILPLEHGSIYIPSSYVDSHHEYPAMTFYSPAVMYSIPS
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                                                 Gaps
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Callithrix jacchus (Common marmoset).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Platyrrhini; Callitrichidae;

Callithrix.
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                 Length
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                 Score 2805; DB 1;
Pred. No. 5.1e-215;
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
88-ERS-COGN RESPECTOR DETAILS (ER-Deta).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R GO; GO: 0005634; C:nucleus; ISS.

R GO; GO: 0005634; C:nucleus; ISS.

R GO; GO: 0005634; C:nucleus; ISS.

R GO; GO: 0005634; F:setrogen receptor activity; ISS.

R GO; GO: 0005480; F:receptor antagonist activity; ISS.

R GO; GO: 0005486; F:receptor antagonist activity; ISS.

R GO; GO: 0005486; F:receptor antagonist activity; ISS.

R GO; GO: 0005486; F:receptor actegors as ignaling pathway; ISS.

R GO; GO: 0005486; F:receptor actegors as ignaling pathway; ISS.

R GO; GO: 0005486; F:receptor actegors activity; ISS.

R GO; GO: 0005486; F:receptor activity; ISS.

R InterPro; IPR001723; Stdhrmu.receptor.

R InterPro; IPR001723; Stdhrmu.receptor.

R InterPro; IPR001656; F:receptor.

R Ffan; PF00106; St. C4steroid.

R PRINTS; PR00047; STRDHORMONER.

R RINTS; PR00047; STRDHORMONER.

R RINTS; RN00439; EAC44; I.

R ROGETTE; RN00399; ZAF C4steroid; I.

R ROGETTE; RN00430; HOLI; I.

R ROGETTE; RN00440; ROGETTE; RN00440; RN04414100; RN04414100.
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SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
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PHOSEPROYLATION (BY SIMILARITY)
PHOSEPROXILATION (BY SIMILARITY)
# 45D89107A84C53D1 CRC64;
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NUCLEAR RECEPTOR-TYPE.
C4-TYPE.
C4-TYPE.
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361 ILDRDEGKCVEGILEVFDMLLATTSRFRELKLQHKEYLCVKAMVLLINSQYDPLVTATQDA 420
                                                                                Drain.";
Submitted (UNN-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Binds estrogens with an affinity similar to that of ER-
-!- FUNCTION: Binds estrogens with an affinity similar to that of ER-
ALPHA, and activates expression of reporter genes containing
estrogen response elements (ERE) in an estrogen-dependent manner.
Isoform 3 and isoform 4 are unable to bind DNA and activate
transcription due to the truncation of the DNA binding domain.
Isoform 2 shows loss of ligand binding affinity and suppresses ER-
                                                          DSSRKLAHLLNAVTDALVWVIAKSGISSQQQSMRLANLIMLLSHVRHASNKGMEHLLNMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Tissue specific responses to estrogen: an explanation based on differential activation of multiple estrogen receptors with different estrogen response elements."; EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning of a novel receptor expressed in rat prostate and ovary."; Proc. Natl. Acad. Sci. U.S.A. 93:5925-5930(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Identification of estrogen receptor beta2, a functional variant estrogen receptor beta expressed in normal rat tissues."; Endocrinology 139:1082-1092(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 46-530 FROM N.A. (ISOFORM 2).
STRAIN=Wistar; TISSUR=Ovary;
MEDLINE=98262932; PubMed=9600083;
MATUPATHA K., Endoh H., Sasaki-Iwacka H., Kanou H., Shimaya E.,
Hashimoto S., Kato S., Kawashima H.;
A novel isoform of rat estrogen receptor beta with 18 amino ac
insertion in the ligand binding domain as a putative dominant
negative regular of estrogen action.";
Blochem. Biophys. Res. Commun. 246:142-147(1998).
                                                                                                                                CKNVVPVYDLILEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSQNPQS 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PARTIAL SEQUENCE FROM N.A. (ISOFORM 5).
STRAIN-Sprague-Dauley; TISSUB-Brain;
Price R., Handa R.J.
"A novel splice variant of estrogen receptor beta found in rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Sprague-Dawley;
MEDLINE=98151005; PubMed=9492041;
Petersen D.N., Tkalcevic G.T., Koza-Taylor P.H., Turi T.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE OF 46-530 FROM N.A. (ISOFORM 1).
SEQUENCE OF 46-530 FROM STRAIN-Sprague-Dawley; TISSUE-Prostate;
MEDLINE-56234066; Pubmed-8650195;
Kuiper G.G.J.M., Enmark E., Pelto-Huikko M., Nilsson S.,
Gustafsson J.-A.;
                                                                                                                                                                                                                                                                     ESR2 RAT STANDARD, PRT; 530 AA. 605936; O35784; O35785; O55015; O55016; O70195; Q9R185; 15-JUL-1999 (Rel. 38, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Estrogen receptor beta (ER-beta). Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 46-530 FROM N.A. (ISOFORMS 1; 3 AND 4).
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STRAIN-Wistar, TISSUE-Prostate,
Aldridge T.C.
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                                                                                                                                                                                                                                                                                                           CAGKAKRSGGHAPRVRELLLDALSPEQLVLTLLEAEPPHVLISRPSAPFTEASWMMSLTK 300
                                                                                                                                                                                                                                                                                                                                             LADKELVHMISWAKKIPGFVELSLFDQVRLLESCWMEVLMMGLWWRSIDHPGKLIFAPDL 360
                                                                                                                                                                                                                                                                                                                                                            LADKELVHMIGWAKKIPGFVELSILDQVRLLESCWMEVLMVGLMWRSIDHPGKLIFAPDL 360
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                                                                                                                                                                                                                                                                                                                                                                                                                DSSRKLAHLLNAVTDALVWVIAKSGISSQQQSMRLANLLMLLSHVRHASNKGMEHLLNMK 480
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                                                                                                                                                                              SSRKLTHINNYDALVWVIAKSGISSQQQSVRLANLIMLLSHVRHISNKGMEHLLSNK
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                                                                                                                                                    Gaps
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PHOSPHORYLATION (BY SIMILARITY).
Missing (in isoform 3 and isoform 4).
                                         Missing (In isoform 5).
/FTida-VSP 003698.
R -> RSSEDPHWHYAQMKSAAPR (in isoform and isoform 4).
/FTida-VSP 003699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CKNVVPVYDLLLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSQNPQSQ 530
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                                                                                                                                   Score 2496; DB 1; Length 530; Pred. No. 1.7e-190;
                                                                                35; Indels
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                                 003697
                                                                                                                                                     27; Mismatches
                                /FTId=VSP
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                                                                                                                     59152 MW;
                                                                                                                                     89.0%;
                                                                                                                                                     468; Conservative
                                                                                  72
150
165
530
87
488
217
                                          318
                                                          364
                                                                                                                     530 AA;
                                                                                                                                             Similarity
                                                                                  72
150
165
505
215
87
488
179
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CONFLICT
CONFLICT
CONFLICT
SEQUENCE
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MOD RES
VARSPLIC
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FUNCTION: Nuclear hormone receptor. Binds estrogens with an affinity similar to that of ESR1 (ER-alpha), and activates expression of reporter genes containing estrogen response elements (ERE) in an estrogen-dependent manner. May play a role in ovarian follicular growth and maturation.

-: SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer with ESR1. Interacts with NCOA3 and NCOA6 coactivators, leading to a strong increase of transcription of target genes. Also interacts with NCOA5 (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY.
MEDLINE=98268825; PubMed=9607809;
Rosenfeld C.S., Ganjam V.K., Taylor J.A., Yuan X., Stiehr J.R.,
Hardy M.P., Lubahn D.B.,
"Transcription and translation of estrogen receptor-beta in the male
"Transcription and wild-type
                                                                                                                                                                        Pettersson K., Grandien K., Kuiper G.G.J.M., Gustafsson J.-A.; "Mouse estrogen receptor beta forms estrogen response element-binding heterodimers with estrogen receptor alpha."; Mol. Endocrinol, 11:1486-1496(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYDRATE-LINKAGE SITE SER-61, AND PHOSPHORYLATION SITE SER-61. MEDLINE-20450734; PubMed=10995528; Cheng X., Cole R.N., Zaia J., Hart G.W.; "Alternative Oglycosylation/O-phosphorylation of the murine estrogen Alternative Oglycosylation/O-phosphorylation."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERACTION WITH NCOA3.
MEDLINB-97336097; PubMed-9192892;
Torchia J., Rose D.W., Inostroza J., Kamei Y., Westin S., Glass C.K.,
Rosenfeld M.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lu B., Leygue B., Dotzlaw H., Murphy L.J., Murphy L.C., Watson P.H., "Estrogen receptor-beta mRNA variants in human and murine tissues."; Mol. Cell. Endocrinol. 138:199-203(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Isolation and characterization of peroxisome proliferator-activated receptor (PPAR) interacting protein (PRIP) as a coactivator for
       Tremblay G.B., Tremblay A., Copeland N.G., Gilbert D.J., Jenkins N. Labrie F., Giguere V., "Cloning, chromosomal localization, and functional analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20250907; Pubmed=10788465;
Zhu Y.-J., Kan L., Qi C., Kanwar Y.S., Yeldandi A.V., Rao M.S.,
Reddy J.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Thetranscriptional co-activator p/CIP binds CBP and mediates
                                                                                                                                                                                                                                                                                                            Leygue E., in B., Dotzlaw H., Glor C., Watson P.H., Murphy Submitted (MAY-1998) to the EWBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                      [4]
SEQUENCE OF 1-60 FROM N.A.
STRAIN-C57BL/6J X 129; TISSUE-Ovary;
ROBENTELL C5.S., Lubahn D.B.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                            46-530 FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                MEDLINE=97424142; PubMed=9280064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALTERNATIVE SPLICING.
TISSUE=Ovary;
MEDLINE=98348389; PubMed=9685228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Endocrinology 139:2982-2987(1998)
                                                                     murine estrogen receptor beta.";
Mol Endocrinol, 11:353-365(1997)
MEDLINE=97211383; PubMed=9058381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        iochemistry 39:11609-11620(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nuclear-receptor function.";
                                                                                                                                                                                                                                                           [3]
SEQUENCE OF 1-60 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor beta.
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TISSUE=Ovary;
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18-08-300-300-7:TBD

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1-- SIBGELLIAME PRODUCTS:

Prent-Alternative Politicing Named and concurses;

Communicadditional isoforms seem to exist;

NamesBet-1:

NamesBet-1:

Signia-005637-1; Sequence-NEP_00369;

NamesBet-5:

Communicadditional isoforms seem to exist;

NamesBet-6:

NamesBet-
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O-LINKED (GLCNAC).  **RSEDEDHWIVAQTKSAVPR (in isoform Bera-2).  **FITIG=USP 001693.** **Missing [in isoform Beta-5).  **FITIG=USP 001694.**  **Missing [in isoform Beta-6).  **FITIG=USP 001696.**  **Missing [in isoform Beta-5A).  **FITIG=USP 001696.**  **MISSING IN SEF 2).  **G-A. IN REF. 2).  **G-A. IN RE	88.9%; Score 2495; DB 1; Length 530; imilarity 88.5%; Pred. No. 2.18-190; Conservative 25; Mismatches 36; Indels 0; Gaps 0; MDIXASPSSINSPSSYNCSQSILPLEHGSIYIPSSYUDSHHEYPAMIPYSPAVMYSIPS 60		i i	VLDRDEGKCVEGILEIFGWILLATTARFREIKUOHKEYLCVKAMILLINSSMYPLATASOEA 420 DSSRKLAHILNAVTDALVWVIAKSGISSQQQSMRLANILMILSHVFHASNKGMEHILNXK 480 :	<pre>tD; PRT; 527 AA. Created) Last sequence update) Last amnotation update) a (ER-beta).</pre>
61 364 364 409 409 105 1139 47 412 412 4415 4415 5101 5101	88 7 88 rvativ SLNSPS	PGROTT PURGIA PVRQTA SGNRCA  :    GGSGCA	NOCTIL NOCTIL GGHAPR             MISWAR MIGWAR	CVEGII	NDA 40, 40, 41, bet;
61 3 64 3 65 3 65 3 19 3 19 1 13 9 1 10 5 1	Similarity 88.5 9; Conservative MDIKMSPSSLWFIEL	NVTNLEGG STGNLEGG STGNLEGG STGNLEGG RETLKRKV RETLKRKLV	NULLICEAL NULLICEAL CAGKAKRS CLINKAKRT LADKELVH LADKELVH LADKELVH		IN STP 29TTS2; 301 (Rel. 301 (Rel. 303 (Rel. receptor
CARBOHYD VARSPLIC VARSPLIC VARSPLIC VARSPLIC MUTAGEN MUTAGEN MUTAGEN CONFLICT	ery Match st Local S cches 469	61 61 121 121		361 421 421 481 481	LT 5 BOVIN BSR2 BOV; Q9XSB5; ( 16-OCT-2( 16-OCT-22 28-FEB-2(
	ក្រឆ្នំ	3 8 5 8 5	6 8 6 8 6 8 6	8 8 8 8 8	RESUL ESR2 1D AC AC DT DT

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Gaps

60 60 240

180

360 357 420 417 480

297

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61 NVTNLEGGPGRQTTSPNVLWPTPGHLSPLVVHRQLSHLYABPQKSPWCEARSLEHTLPVN 120
                                                                                                                                                                                                                                                                                                                                                                                                                              --NSEDGPGRQTISPNVIMPTPGHLSPLAIHCQPSVLYARPQKSPWRETRSLEHTLPVN 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGKAKRSGGHAPRVRELLILDALSPEQLVLTLLEAEPPHVLISRPSAPFTEASNAMSLTK 300
                                                                                                                                                                                                                                                                                                                                           1 MDVKNSPSSLMSPVSYNCGQSILPLEPGPIYLPSSYVESRHEYSAVTFYSPAVMYSIPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  418 DSGRKLTHLLINAVTDALVWVIAKSGMSSQQQSWRLANLIMLLSHVRHASNKGMEHILINWK
                                                                                                                                                                                                                                                                                                             1 MDIKNSPSSINSPSSYNCSQSILPLEHGSIYIPSSYVDSHHBYPAMTFYSPAVMNYSIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 NDYICPATNOCTIDKNRRKSCQACRLRKCYEVGMVKCGSRRERCGYRLVRRQRSADBQLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 CLSKTKRNGGPMTRVKELLISALSPEQLVLTLIEAEPPHVLISRPSTPFTEASMMMSLTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 LADKELVHMISWAKKIPGFVELSLFDQVRLLESCWMEVLAMGLMWRSIDHPGKLIFAPDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 LADKELVEMISWAKKIPGEVELSLYDQVRLLESCWLEVEMYGLMYMSIDHPGKLIFAPDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 VLDRDEGKCVEGILEIFDMLLATTSRPRELKLQHKEYLCVKAMILLNSSMYPLVTATQDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 DSSRKLAHLLNAVIDALVWVIAKSGISSQQQSWRLANLLMLLSHVRHASNKGMEHLLNMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 RETLKRKVSGNRCASPVTGPGSKRDAHFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ovis aries (Sheep).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         481 CKNVVPVYDLLLEMIANAHVLRGCKSSITGSECSPAEDSKSKEGSQNPQSQ 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     478 CKAVVPVYDLILEMIANAHTLAGNKSLVTGSERNIVEDSESKEGSQKPQAQ 527
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Biol. Reprod. 65:128-134(2001).
-!- FUNCTION: Nuclear hormone receptor. Binds estrogens with an
                                                                                                                                                                                                                                                                <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS BETA AND BETA-1).
TISSUE-Ovary;
MEDLINE=2131342; PubMed=11420232;
Cardenas H., Burke K.A., Bigaby R.M., Pope W.F., Nephew K.P.,
"Estrogen receptor beta in the sheep ovary during the estrous
                                               C4-TYPE.
STEROID-BINDING.
PHOSPHORYLATION (BY SIMILARITY)
PHOSPHORYLATION (BY SIMILARITY)
N -> D (IN REF. 2)
9CEPFEIO6F4E4C84 (RC64;
                                                                                                                                                                                                                   DB 1; Length
                                                                                                                                                                                                                                                             39; Indels
  NUCLEAR RECEPTOR-TYPE.
C4-TYPE.
                                                                                                                                                                                                                ; Score 2463.5; DB 1; Pred. No. 6.6e-188; 22; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09TUIS; 09N0T6;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
BSR2 OR NR3A2.
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                                                    182
212
84
485
60
527 AA;
                                                                                                                                                                                                                                            Similarity
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       DNA BIND
ZN FING
ZN FING
DOMAIN
MOD RES
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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                                                                                                                                                                                                                     Query Match
Best Local
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ESR2_SHEEP
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Matches
          EEEEEE88
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                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 4-527 FROM N.A.

MEDLINES-995-9179; PubMed=10432221;
Walther N., Lioutas C., Tillmann G., Ivell R.;
"Cloning of bovine estrogen receptor beta (Erbeta): expression of
novel delaced insoforms in reproductive tissues.";
Mol. Cell. Endocrinol. 152-137-45(1999).
-!- FUNCTION: Nuclear hormone receptor. Binds estrogens with an
affinity similar to that of ESR1 (ERR-alpha), and activates
expression of reporter genes conclaining estrogen response elements
(ERR) in an estrogen-dependent manner. May play a role in ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity).

SUBCELLUIAR LOCATION: Nuclear.

TISSUE SPECIFICITY: Present in granulosa cells of antral follicles in various stages of follicular growth.

DOMAIN: Composed of three domains: a modulating N-terminal domain, a DNA-binding domain and a C-terminal steroid-binding domain similarial steroid-binding domain.

SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R GO; GO:0005634; Crucleus; ISS.

R GO; GO:0005634; Crucleus; ISS.

R GO; GO:0006491; F:estrogen receptor activity; ISS.

R GO; GO:00048019; F:receptor antagonist activity; ISS.

R GO; GO:0005496; F:stecroid binding; ISS.

R GO; GO:0005496; F:stecroid binding; ISS.

R GO; GO:00030308; P:receptor asignaling pathway; ISS.

R GO; GO:0030308; P:regulation of call growth; ISS.

R GO; GO:00030308; P:regulation of transcription, DNA-dependent; ISS.

R Interpro; IPR000355; Hormon_receptor.

R Interpro; IPR001323; Stdhrmn_receptor.

R Interpro; IPR001646; Str_ncl_receptor.

R Interpro; IPR00165; Zfr_C4; I.

R Pfam; PR00105; zf-C4; I.
                                                                                                                                                                                                                                                                                            "Cloning, sequencing, and localization of bovine estrogen receptor-
beta within the ovarian follicle.";
Biol. Reprod. 60:691-697(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       with
                                                                                                                                                                                            STRAIN-Hoistein; TISSUE=Ovarian follicle;
MEDLINE=99150196; PubMed=10026117;
Rosenfeld C.S., Yuan X., Manikkam M., Calder M.D., Garverick H.A.,
                                   Bos taurus (Bovine).
Makaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinee; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00393; STROIDFINGER.
PRINTS; PR00047; STROIDFINGER.
ProDom; PD000035; ZnE C4steroid; 1.
SWART; SM0039; ZnE C4; 1.
SWART; SM0039; ZnE C4; 1.
PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
Zinc-finger; Transcription regulation; DNA-binding; Nuclear protein; DOMAIN: 1 145 MODULATING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 follicular growth and maturation.
SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer BERI. Interacts with NCOA3, NCOA5 and NCOA6 coactivators, to a strong increase of transcription of target genes (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, AF110402, AAD24432.1; -. EMBL, Y18017; CAB53861.1; ALT_INIT. HSSP; P03372; 1HCQ.
                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 subfamily.
            ESR2 OR NR3A2
                                                                                                                                                                                                                                                                          Lubahn D.B.;
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---NSEDGFGRQTTSPNVLMPTPGHISPLAIHCQSSLLYARPQKSPWCETRSLRHTPPVN

1 MDVKNSPSSLNSPVSYNCGQSILPLEPGPIYLPSSYVESRHEYSAVTFYSPAVMNYSIPN NVTNLEGGPGROTISPNVLWPTPGHLSPLVVHRQLSHLYABPOKSPWCBARSLEHTLPVN NDYICPATNOCTIDIONRRKSCOACRLRKCYEVGMVKCGSRRERCGYRLVRRQRSADEQLH 240

178 NDYICPATNQCTIDKNRRKSCQACRLRKCYBVGAVYKCGSRRBRCGYRIVRRQRNSDEQLH

RETLIKRIKASGSSCASPVSSPSSKRDAHPCAVCSDYASGYHYGVWSCEGCKAPFKRSIQGH

RETLIKRKVSGNRCAS PVTGPGSKRDAHFCAVCSDYASGYHYGVWSCEGCKAFFKRS I QGH

121 118 181

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CAGKAKRSGGHAPRVRELLLDALSPEQLVLTLLEASPPHVLISRPSAPFTEASMMMSLTK 300 CLSKTKRNGAPMTRVKELLISALSPEQLVLTLIEAEPPHVLMSRPSAPFTEASMMSLTK 297

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CKNVVPVYDLLLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSQNPQSQ 530 CKNVVPVYDLILEMLNAHTLRSNKPLVTRSERNLAEDSESKEGSQKPQAQ 527 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. NCBI_TaxID=9823;

[1] SEQUENCE FROM N.A.

Sus scrofa (Pig)

BSR2 PIG STANDARD; PRT; 526 AA. 09XSW2; 09BDW5; 16-OCT-2001 (Rel. 40, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Estrogen receptor beta (BR-beta).

and

TISSUE=Embryo;

Kowalski A.A., Graddy L.G., Vale-Cruz D.S., Choi I.,

Katzenellenbogen B.S., Simmen F.A., Simmen R.C.M.;

"Molecular cloning of porcine estrogen receptor beta cDNAs developmental expression in peri-implantation embryos.";

Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

SECUENCE FROM N.A.

DSSRKILAHILINAVTDALVWVIAKSGISSQQSMRLANLIMILISHVRHASNKGMEHLINMK 480

VLDRDBGKCVEGILEIFDMLLATTSRPRELKLQHKEYLCVKAMILLNSSMYPLVTATQDA

LADKELVHMISWAKKIPGFVELSLYDQVRLLESCWLEVLMVGLMWRSIDHPGKLIFAPDL 357

LADKELVHMISWAKKI PGFVELSLPDQVRLLBSCWMEVLMMGLMWRSIDHPGKLI FAPDL

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                                                                                                                                                                                                                                                                                                                                                                             IsoId=09TU15-2; Sequence=VSP 003700, VSP 003701; Orongosed of three domains: a modulating N-terminal domain, a DNA-binding domain and a C-terminal steroid-binding domain. SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hissi, 1903-02.

Hissi, 1903-03.

Hissi, 1903-03.

Hissi, 1900-03.

Hissi,
affinity similar to that of BSR1, and activates expression of reporter genes containing estrogen response elements (BRB) in an estrogen-dependent manner.
SUBGNIT: Binds DNA as a homodimer. Can form a heterodimer with ESR1. Interacts with NCOA3, NCOA3 and NCOA6 coactivators, leading to a strong increase of transcription of target genes (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Steroid-binding; Alternative splicing; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C4-TYPE.
C4-TYPE.
STEROID-BINDING.
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
FUELSLYDQ. -> MKGNVLKEF (in isoform
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Missing (In isoform Beta-1).
/FIId=VSP 003701.
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NUCLEAR RECEPTOR-TYPE.
                                                                                                                                                                                                                                               Svent=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.5%; Score 2455.5; DB 1
87.5%; Pred. No. 2.8e-187;
iive 24; Mismatches 39;
                                                                                                                                                                                                                                                                                                                             IsoId=Q9TU15-1; Sequence=Displayed;
                                                                                                                                                                                         SUBCELLULAR LOCATION: Nuclear ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF177936; AAD55772.1; -. EMBL; AF257109; AAF71745.1; -.
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                                                                                                                                                                                                                                                                                                                                                         Name=Beta-1;
                                                                                                                                                                  similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       subfamily.
                                                                                                                                                                                                                                                                                                   Name=Beta;
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VARSPLIC
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porcine ovary.";
Submitted (MRX-2001) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: Nuclear hormone receptor. Binds estrogens with an affinity similar to that of ESR1 (ER-alpha), and activates expression of reporter genes containing estrogen response elements (ERE) in an estrogendent manner. May play a role in ovarian follicular growth and maturation.
-!-SUBMIT: Binds DMA as a homodimer. Can form a heterodimer with Inceracts with NCOA3, NCOA5 and NCOA6 coactivators, leading to a strong increase of transcription of target genes (By
                                                                                                                                                                                                                                                                                         IISSUB=Ovary;
LaVoie H.A., DeSimone D.C.;
cloning and expression of estrogen receptor beta isoforms from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
SUBCELLULAR LOCATION: Nuclear.
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3; Gaps

DB 1; Length 527; 39; Indels 1 MDIKNSPSSLNSPSSYNCSQSILPLEHGSIYIPSSYVDSHHEYPAMTFYSPAVMNYSIPS 

Conservative

Local Similarity

Query Match

Matches 464;

us-08-906-365-2.rsp

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                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NVTNLEGGPGROTTSPNVLMPTPGHLSPLVVHROLSHLYARPQKSPWCBARSLEHTLPVN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --NEVGPGRQATSPNVLWPTPGHLSPLAIHCQPSLLYARPQKSPWCDTRSLEHTLPVN 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RETLIKRKVSGNRCASPVTGPGSKRDAHFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RETLKRKASGSSCASPVTSPSSKRDAHFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGH 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NDYICPATNQCTIDKONRRKSCQACRLRKCYEVGMVKCGSRRERCGYRLVRRQRSADEQLH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 NDYICPATNQCTIDKARRAKSCQACRLRKCY3VGAVKCGSRRERCGYRIVRKQRNSEGHLH 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGKAKRSGGHAPRVRELLLDALSPEQLVLTLLEASPPHVLISRPSAPFTEASMMSLTK 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60
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DOMAIN: Composed of three domains: a modulating N-terminal domain, a DNA-binding domain and a C-terminal steroid-binding domain. SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
                                                                                                                                                                                                 EVEL, APIGABS, AND45381.2;

EVEL, APIGABS, AAM15181.1;

EVEL, APIGABS, AAM15181.2;

EVEL, APIGABS, AAM15181.1;

EVEL, APIGABS, AAM15181.1;

EVEL, APIGABS, AAM15181.1;

EVEL, APIGABS, EVELOPER AND EVELOPER TO EV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MDIKUSPSNINSPVSYNCSQSVLPLEPGPIYIPSSYVESCHEYSAMTFYSPAVVNXSISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MDIKNSPSSLNSPSSYNCSOSILPLEHGSIYIPSSYVDSHHEYPAMTFYSPAVMVKSIPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40; Indels
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STENDID-BINDING (BY SIMILAR:
PHOSPHORYLATION (BY SIMILAR:
PHOSPHORYLATION (BY SIMILAR:
M - V (IN REF. 2).
T -> M (IN REF. 2).
W; 35CEDP6610788F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tch 86.1%; Score 2415; DB 1; al Similarity 86.2%; Pred. No. 4.7e-184; 457; Conservative 29; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58849 MW;
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166
206
526
84
484
469
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146 1
182 2
212 8
484 4
484 4
317 3
469 4
                                                  subfamily
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DIA BIND
DIA FING
ZIN FING
ZIN FING
DOMAIN
MOD_RES
MOD_RES
CONFLICT
CONFLICT
SEQUENCE
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Best Local
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                                           298 LADKELVHMISWAKKIPGFMELSLYDQVRLLESCWLEVLMVGLMWRSIDHPGKLIFAPDL 357
                                                                                                                                              420
                                                                                                                                                                                                                 416
                                                                                                                                                                                                                                                                                         DSSRKILAHILINAVTDALVWVIAKSGISSQQQSMRLANILLMLLSHVRHASNKGMEHLLINKK 480
                                                                                                                                                                                                                                                                                                                                417 ESSRKITHILIMAYTDALVWYTARSGISSQQQSVRLANILMLLSHVRHASNKGTEHLLMWK 476
LADKELVHMISWAXKIPGFVELSLFDQVRLLESCWMBVLMMGLMWRSIDHPGKLIFAPDL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBUNIT: BINDS DNA AS A HOMODIMER. CAN FORM A HETERODIMER WITH ERALFA (BY SIMILARITY).
-!- SUBCELLULAR LOCATION.
-!- SUBCELLULAR LOCATION.
-!- TISSUB SPECIFICITY: BRAIN, PITUITARY, SKELETAL MUSCLE, LIVER, ADREMAL, KIDNEY, INTESTINE, AND OVARY.
-!- DOMAIN: Composed of three domains: a modulating N-terminal domain, a DNA-binding domain and a C-terminal steroid-binding domain.
-!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Brain,
MEDLINE=94277866; PubMed=10499520;
Bernard D.J., Bentley G.E., Balthazart J., Turek F.W., Ball G.F.;
Bernard D.J., Bentley G.E., Balthazart J., Turek F.W., Ball G.F.;
"Androgen receptor, estrogen receptor alpha, and estrogen receptor
beta show distribute patterns of expression in forebrain song control
unclei of European starlings.";
Endocrinology 140:4633-4643(1999).
-! FUNCTION: BINDS ESTROGENS WITH AN AFFINITY SIMILAR TO THAT OF ER-
-I-FUNCTION: BINDS ESTROGENS WITH AN AFFINITY SIMILAR TO THAT OF ER-
ALPHA, AND ACTIVATES ELEMENTS (ERE) IN AN ESTROGEN-DEPENDENT MANNER.
LOCALLY SYNTHESIZED ESTROGENS MAY ACT VIA ER BETA, IN ADDITION TO
ER ALPHA, TO MEDIATE SEASONAL OR DEVELOPMENTAL EFFECTS ON NEARBY
SONG NUCLEI.
                                                                                                                                                                                      VLDRDEGKCVEGILEIFDMILATTSRFRELKLQHKEYLCVKAMILLNSSMYPLVTATQDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF113513; AAD56593.1; -.
HSSP; P03372; IHCQ.
GO; GO:0005634; C:nucleus; ISS.
GO; GO:00130284; F:estrogen receptor activity; ISS.
GO; GO:00048019; F:isterogen antagoniet activity; ISS.
GO; GO:0005496; F:steroid binding; ISS.
GO; GO:0005520; F:steroid binding; ISS.
GO; GO:0005520; F:steroid binding; ISS.
GO; GO:000555; F:estrogen receptor signaling pathway; ISS.
GO; GO:000555; F:regulation of transcription, DNA-dependent; ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sturnus valgaris (Starling).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Archosauria, Aves, Neognathae, Passeriformes, Sturnidae, Sturnus.
                                                                                                                                                                                                                                                                                                                                                                                                                                               CKNVVPVYDLLLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSONPOSO 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           477 CKNVVPVYDLLLEMLANAHTLRGNKSLVTGSERSRMEESESKEGSQKPQAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9172;
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                                                                                                                                                          361
       301
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DNA BIND
ZN FING
ZN FING
DOMAIN
SEQUENCE
     DSSRXIAHILINAVTDALVWVIAKSGISSQQOSMRLANLIMLLSHVRHASNKGMEHLINWK 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 NDYICPATNQCTIDKNRRKSCQACRLRKCYEVGMVKCGSRRERCGYRLVRQRSADBQLH 240
206 NDXICPATNQCTIDKNRRKSCQACRLRKCYEVGMMKCGSRRERCGYRLLRSHRGARERVH 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           266 CLGRARRYSBAATRVKEILLSTVSPEQFVLTLLEAEPPHVLVSRPSKPFTEASWMSLITK 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LADKELVHMISWAKKIPGFVELSLFDQVRLLESCWMEVLAMGLMWRSIDHPGKLIFAPDL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VLDRDEGKCVEGILEIFDMLLATTSRFRELKLOHKEYLCVKAMILLNSSMYPLVTATODA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    386 VLDRDBGKCVBGILEIFDMLAMTSRFRELKLQHKBYLCVKAMILLNSSMFPL--SAEEP 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 VINLEGGERGITSPNVIMPTPGHLSPLVVHRQLSHLYAEPOKSPWCEARSLEHTLPVNR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGKAKRSGGHAPRVRELLLDALSPEQLVLTLLEAEPPHVLISRPSAPFTEASMMSLTK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 DIKNSPSSLNSPSSYNCSQSILPLEHGSIYIPSSYVDSHHEYPAMTFYSPAVMNYSIPSN 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000536; Hormone_rec_lig.

InterPro; IPR001723; Stdhrmn_receptor.

InterPro; IPR001828; Ztdhrmn_receptor.

InterPro; IPR001828; Ztf_Cateroid.

R Pfam; PF00104; hormone_rec; 1.

R Pfam; PF00105; zf-C4; T.

R RINTS; PR00398; STRDHORMONER.

R PRINTS; PR00398; STRDHORMONER.

R PRODOM; PD000035; Zmf_C4; I.

SMART; SM00430; Zmf_C4; I.

R SMART; SM00399; Zmf_C4; I.

R ROSTTE; PS00031; NÜCLEAR_RECEPTOR; I.

R RECEPTOR; Tanscription regulation; DNA-binding; Nuclear protein;
Zinc-finger; Steroid-binding.

M DOMAIN

Z DOMAIN

Z DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                           4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESR2 COTJA STANDARD; PRT; 472 AA.
093511;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CKNVVPVYDLLLEMLNAHVLRGCKSSI - TGSECSPAEDSKSKEGSQNPQSQ 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     504 CKNVVPVYDLILEMINAHTLRGQRKPLATHPBPGPLEQMEPGESLRKGBPQ 554
                                                                                                                                                                                                                                                                                                                                                                                      Length 554;
                                                                                                                                                                                                                                                                                                                                                                                                                           80; Indels
                                                                                                                                                                                                                                                                        174 239 NUCLEAR RECEPTOR-TYPE.
174 194 C4-TYPE.
210 234 C4-TYPE.
240 554 STERCID-BINDING.
554 AA; 62173 MW; EC13A961CEBE59C9 CRC64;
                                                                                                                                                                                                                                                         MODULATING.
NUCLEAR RECEPTOR-TYPE.
C4-TYPE.
C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
74.9%; Score 2101; DB 1;
Best Local Similarity 74.8%; Pred. No. 4.2e-159;
Matches 397; Conservative 50; Mismatches 80;
                                                                                                                                                                                                                                                                          DNA BIND
ZN FING
ZN FING
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56
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                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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ESR2_CO
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                SEQUENCE FROM N.A.
Foidart A., Lakaye B., Grisar T., Ball G.F., Balthazart J.;
"Sequence and neuroanatomical distribution of estrogen receptor beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lakaye B., Foldart A., Grisar T., Balthazart J.;
"Partial cloning and distribution of estrogen receptor beta in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0398; STRDHORMONER.
PRINTS; PRO0047; STROIDFINGER.
PRODOM; PRO000035; SAI_C4steroid; 1.
SWART; SM00430; HOLI; 1.
SWART; SM00439; ZAF_C4; 1.
SWART; SM00399; ZAF_C4; 1.
SWART; STROIDFINGER.
RECEPTOR; Transcription regulation; DNA-binding; Nuclear protein; Zinc-finger; Steroid-binding.
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Pred. No. 6.4e-148;
                                                                                                                                                                                                                                                                                                                  in the quail brain.";
Submitted (SEP-1998) to the EMBE/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STEROID-BINDING.
DF7A78F0FDBD18BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MODULATING.
NUCLEAR RECEPTOR-TYPE.
C4-TYPE.
C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Testis;
MEDLINE=98430913; PubMed=9760113;
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80.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 141-286 FROM N.A.
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141
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472 AA;
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Best Local Similarity
                                                            Coturnix.
NCBI_TaxID=93934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         avian brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                subfamily.
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PWCBARSLEHTLPVNRETLXRKVSGNRCASPV-TGPGSKRDAHFCAVCSDYASGYHYGVW 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 PWCEVRPLDPVLPVTRETLKRKTNGSDCTSPIASNPGSKRDAHFCAVCSDYASGYHYGVW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCEGCKAPPKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLRKCYEVGMVKCGSRRERC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GYRLVRRQRSADEQLHCAGKAKRSGGHAPRVRELLLDALSPEQLVLTLLBABPPHVLISR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSAPFTEASMMMSLTKLADKELVHM1SWAKKIPGFVELSLFDQVRLLESCWMEVLMMGLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238 PSKPFTEASMAMSLTKLADKELVFMIGWAKKIPGPIDLSLYDQVRLLBSCWMBVLMIGLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46 MTFYSPAVMNYSIPSNVTNLEGGPGRQTTSPNVLMPTPGHLSPLVVHRQLSHLYAEPQKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              358 LINSSMPPL--SPEEPESNRKLHHILANVYDALVWVIAKSGIPSQQQTTRLANLLAHLISH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                345 WRSIDHPGKLIFAPDLVLDRDEGKCVBGILBIFDWLLATTSRFRELKLQHKEYLCVKAMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298 WRSIDHPGKLIFAPDLVLDRDSGKCVBGILEIFDMLLAMTSRFRELKLQHKEYLCVKAMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LINSSMYPLVTATQDADSSRKLAHLLMAVTDALVWVIAKSGISSQQQSMRLANLLMLLSH
ESR2 ANGJA STANDARD; PRT; 573 AA.
013012;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last sequence elements)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last a
                                                                                                                                                                                                                                                                                                                                                                                                                                              69.5%; Score 1948.5; DB 1; Length 472; 79.3%; Pred. No. 4.4e-147; ive 38; Mismatches 52; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VRHASNKGMEHILAMKCKNVVPVYDLLLEMLNAHVIRG-CKSSITGSE 511
                                                                                                                                                                                                                                                                                                                                                                                           STEROID-BINDING.
MW; ABCBBBCACA65650 CRC64;
                                                                                                                                                                                                                                                                                                                     MODULATING.
NUCLEAR RECEPTOR-TYPE.
C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                             C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                  53439
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165
472
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105
141
171
472 AA;
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ZN FING
ZN FING
DOMAIN
SEQUENCE
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Best Local 8
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                         e.
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                                                             105
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                                                                                                                                                        SCEGCKAFFKRSIQGHNDYICPATNOCTIDKNRKSCQACRLRKCYEVGMVKCGSRRERC 224
                                                                                                                                                                                                                                  SCEGCKAPFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLRKCYEVGMMKGGSRRERC 180
                                                                                                                                                                                                                                                                                     GYRLVRRQRSADEQLHCAGKAKRSGGHAPRVRELLLDALSPEQLVLTLLBAEPPHVLISR 284
                                                                                                                                                                                                                                                                                                                         237
                                                                                                                                                                                                                                                                                                                                                               PSAPFTEASMMMSLTKLADKELVHMISWAKKIPGFVELSLFDQVRLLESCWMBVLMMGLM 344
                                                                                                                                                                                                                                                                                                                                                                                   298 WRSIDHPGKLIFAPDLVLDRDEGKCVEGILEIFDMLLAMFSRFRELKLQHKEYLCVKAMI 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLNSSMYPLVTATODADSSRKLAHLLNAVTDALVWVIAKSGISSOOOSMRLANLLMLLSH 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-White leghorn; TISSUE-Testis;
STRAIN-White leghorn; TISSUE-Testis;
Suzuki M., Mizuno S., Nakabayashi O.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
-!-FUMCTION: BINDS BSTROGENS WITH AN APPINITY SIMILAR TO THAT OF
ER-ALPHA, AND ACTIVATES EXPRESSION OF REPORTER GENES CONTAINING
ESTROGEN RESPONSE BLEMENTS (ERB) IN AN ESTROGEN-DEPENDENT MANNER.
-!-SUBUNIT: BINDS DNA AS A HOMODIMER. CAN FORM A HETERODIMER MITH BR-
ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain,
                                                                                   PWCBARSLEHTLPVNRETLKRKVSGNRCASPV-TGPGSKRDAHFCAVCSDYASGYHYGVW
                                                                                                                                                                                                                                                                                                         WRSIDHPCKLIFAPDLVLDRDEGKCVEGILBIFDMLLATTSRFRBIKLQHKBYLCVKAMI
                                                               46 MTFYSPAVANYSIPSNVTNLEGGPGROTISPNVLWPIPGHLSPLVVHROLSHLYARPQKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Nuclear.

DOWAIN: Composed of three domains: a modulating N-terminal domain and N-binding domain.

SIMILARITY: Belongs to the nuclear hormone receptor family. NR3 subfamily.
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                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VRHASNKGMEHLLINMKCKNVVPVYDLLLEMLNAHVLRGCKSS
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                           47:
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ESTZOGEN RESEQUENCE (ER-beta) (CERb).
                         Mismatches
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                           39;
                           370; Conservative
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                             Matches
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Gaps

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105

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224

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TLKRKVSGNRCASPVTGPGS----KRDAHFCAVCSDYASGYHYGVWSCEGCKAFFKR
                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Last sequence update) 28-FBB-2003 (Rel. 41, Last annotation update) Estrogen receptor beta-1 (ER-beta-1). Carassius auratus (Goldfish).
                                                                                                                                                                                                                                                                                                                                                                                 568 A.A.
                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                         SQ 530
                                                                                                                                                                                                                                                                                                                               SQ 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            subfamily.
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                                                                                                                                                                                                                                                                                                                                                                                  ERB1 CARAU
Q9W669;
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ERB1_CARAU
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                                                                                                                                                                                                                                                                                                                      137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----GRQTTSPNVLWPT----PGHLSPLVVHRQLSHLYAEPQKSPWCEARSLEHTLPVNRE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSSYNCSOSILPLEHGSIYIPSSYVDSHHEYPAMTFYSPAVMYSIPSNVTNLEGGP--- 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82
                                                                                      MOI. Cell. Endocrinol. 119:37-45(1996).
-!- FUNCTION: BINDS ESTROGENS WITH AN AFFINITY SIMILAR TO THAT OF
ER-ALPHA, AND ACTIVATES EXPRESSION OF REPORTER GENES CONTAINING
ESTROGEN RESPONSE ELEMENTS (ERE) IN AN ESTROGEN-DEPENDENT MANNER.
-!- SUBUNIT: BINDS DNA AS A HOMODIMER, CAN FORM A HETERODIMER WITH ER-
                                                                                                                                                      -!- SUBCELLULAR LOCATION: Nuclear.
-!- TISSUB SPECIFICITY: Liver.
-!- INDUCTION: By 17-beta-estradiol.
-!- DOMAIN: Composed of three domains: a modulating N-terminal domain, a DNA-binding domain and a C-terminal steroid-binding domain.
-!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESPAAROSLSPSLFWPAHGHHGHVSPLALHFQOPLVYREPAHSPWAEPKDLEH-----GQ
                                                                                                                                                                                                                                                                                                                                                  46; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0398; STRDHORNONER.
PRONTS; PRO0404; STROIDFINGER.
ProDom; PD000035; ZnE C4steroid; 1.
SMART; SM00399; ZnE C4; 1.
SMART; SM00399; ZnE C4; 1.
SMART; SM00391; NUCLEAR RECEPTOR; 1.
Receptor; Transcription regulation; DNA-binding; Nuclear protein;
                                                                   estrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.2%; Score 1549; DB 1; Length 5
larity 57.7%; Pred. No. 3e-115;
Conservative 62; Mismatches 121; Indels
                                                        Todo T., Adachi S., Yamauchi K.; "Molecular cloning and characterization of Japanese eel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STEROID-BINDING.
9C64CIDBD39ED4CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEAR RECEPTOR-TYPE C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MODULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C4-TYPE.
                        SEQUENCE FROM N.A.
TISSUE=Liver;
MEDLINE=96386022; PubMed=8793852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63420 MW;
                                                                                                                                                                                                                                                                                                                                EMBL; AB003356; BAA19851.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Steroid-binding.
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207
237
573 AA;
                                                                                                                                                                                                                                                                                                                                            P03372; 1HCO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 313; Conserv
                                                                               CDNA. ";
   NCBI_TaxID=7937;
                                                                                                                                                                                                                        subfamily.
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DOMAIN
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SEQUENCE
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A MEDLINE=916917; PubMed=10068500;

Thoudakova A.V., Pathak S., Callard G.V.;

Troundakova A.V., Pathak S., Callard G.V.;

Troundakova A.V., Pathak S., Callard G.V.;

Troundakova A.V., Pathak S., Callard G.V.;

Gon Comp. Endocrinol. 1113:389-400(1999)

C. -- FUNCTION: BINDS ESTROGENS WITH AN APFINITY SIMILAR TO THAT OF ESTROCEN RESPONSE ELEMENTS (ERE) IN AN ESTROGEN-DEPENDENT MANNER.

C. -- SUBJUIT: BINDS DNA AS A HOMODIMER. CAN FORM A HETERODIMER WITH ER-ALPHA (BY SIMILARITY).

C. -- SUBJUILARITY: A HOMODIMER. CAN FORM A HETERODIMER WITH ER-ALPHA (BY SIMILARITY).

C. -- DOMAIN: Composed of three domains: a modulating N-terminal domain, a DNA-binding domain and a C-terminal steroid-binding domain.

C. -- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
                                                                                                                                                                                                                                                                                                    349
SIQGHNDYICPATNQCTIDKNRRKSCQACRLRKCYEVGMVKCGSRRERCGYRLVRRQRSA 235
                                                                                                                                                236 D--EQLHCAGKA---KRSGGHAPRVRELLLDALSPEQLVLTLLEAEPPHV-LISRPSAPF 289
                                                                                                                                                                                                                            317
                                                                                                                                                                                                                                                                                                                                                    409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                410 MYPLVTAT-QDADSSRKLAHLLNAVTDALVWVIAKSGISSQQQSMRLANILMLISHVRHA 468
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                                                                                                                                                                                                                                                                                                        TRASMAMSLTKLADKELVHMISWAKKIPGFVELSLFDQVRLLESCWMEVLMMGLMWRSID
                                                                                                                                                                                                                                                                                                                                                                                                                                                        350 HPGKLIFAPDLVLDRDEGKCVEGILEIFDMLLATTSRFRELKLQHKEYLCVKAMILLNSS
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                                                                                                                                                                                                                            258 HIRELAGTGGGARTORRGEGVVPOTOEAOSSALTPEOLINRIIEAEPPEIYLMKELKKPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Cdoldfish).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopierygii, Teleostei, Ostariophysi, Cypriniformes,
Cyprinidae, Carassius.

NCBI_TaxID=7957;
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DNA BIND
ZN FING
ZN FING
DOMAIN
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 211 QCTIDKNRRKSCQACRIRKCYEVGWMKCGLRRDRSSY----QQRGAQQNRLTRFSGRMRT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 OCTIDKNERKSCQACRLEKCYEVGMVKCGSRREROGYRLVRRQRSADEQ--LHCAGKAKR 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIKILADKELVIMISWAKKIPGFVELSLPDQVRLLESCWMEVLMMGLMWRSIDHPGKLIFA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDIVIDRDEGKCVEGILEIFDMLLATTSRFRELKIQHKEYLCVKAMILINSSM-YPLVTA 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TODADSSRKLAHLINAVTDALVWVIAKSGISSQQQSMRLANLIMLLSHVRHASNKGMEHL 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCCHAPRVR------ELLLDALSPEQLVLTLIEAEPPHV-LISRPSAPFTEASMMS 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                     92
                                                                                                                                                                                                                                                                                                                                                                                                                                           38 SP-TFNSSSPSLDVESHPICIPSPYTDLGHDFTTLPFYSPSLLGY----GTSPLSDCPSV
                                                                                                                                                                                                                                                                                                                                                                                                                       SPSSYNCSOSILPLEHGSIXIPSSYVDSHHEYPAMTEYSPAVMYSIPSWVTNLEGGPG-
    | HSSPP p033721 IERR. | InterPro; IRR001023; Stdhrmn_receptor. | InterPro; IRR001023; Stdhrmn_receptor. | InterPro; IRR001068; Str_ncl_receptor. | InterPro; IRR001068; Str_ncl_receptor. | InterPro; IRR001068; Str_ncl_receptor. | InterPro; IRR001069; Str_ncl_receptor. | InterPro; IRR001069; STRENCRER. | Fam: PP001069; STRENCRER. | PRINTS; PR00049; STRENCRER. | PRODOW; STRENCRER. | PRODOW; STROIDFINGER. | PRODOW; STROIDFINGER. | PROSITE; SM00430; HGJI, 1. | SWART; SM00430; HGJI, 1. | SWART; SM00430; HGJI, 1. | It is now in the second of the
                                                                                                                                                                                                                                                                                                                                                                                          26;
                                                                                                                                                                                                                                                                                                                                                          52.3%; Score 1466; DB 1; Length 568; 56.0%; Pred. No. 1.1e-108; ive 75; Mismatches 127; Indels 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 477 LINKKCKNVVPVYDLLLEMINAHVLRGCKSSITGSECSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESR2_ONCMY STANDARD; PRT; 568 AA. P57782.
P57782.
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
18-COCT-2001 (Rel. 40, Last annotation update)
18-RSR2 OR NR3A2.
                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 56.00
Matches 290; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lb.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75 SPNVLWPTPGHLSPLVVHRQLSHLYA-EPQKSPWCEARSLEHTLPVNRETLKRKVSGNRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 YNCSQSILPLEHGSIXIPSSYVDSHHEYPAMTFYSPAVMY-SIPSNVTNLEGGPGRQTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 ASPVIGEGSKRDAHFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPAINQCTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ28983; CAC66714.1; -.

R HSSP; P03372; 1ERR.

R InterPro; 1PR000536; Hormone_rec_lig.

R InterPro; 1PR001628; Suffirm_receptor.

R InterPro; 1PR001628; Suf_C4steroid.

R Pfam; PF00104; hormone_rec; 1.

R Pfam; PF00104; APC10FINCER.

R PRINTS; PR00399; STRDHORMONER.

R PRINTS; PR00399; STRDHORMONER.

R PRINTS; PR000399; Zuf_C4steroid; 1.

SMART; SM00430; HOLI; 1.

R SMART; SM00430; HOLI; 1.

R PROSITE; PS00031; WIGLEAR RECEPTOR; 1.

R RECEPTOR; Transcription regulation; DNA-binding; Nuclear protein; M Zinc-finger; Steroid-binding, Mountains
                                                                                                                                                                                                                    Haugg M., Ackermann G., Fent K.,
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.4%; Score 1440.5; DB 1; Length 568; 54.9%; Pred. No. 1.2e-106; ive 85; Mismatches 121; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MODULATING.

NUCLEAR RECEPTOR-TYPE.

C4-TYPE.

C4-TYPE.

STEROID-BINDING.
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178 198 C4-
214 288 C4-
244 568 STE
568 AA, 63813 NW; F
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Best Local Similarity 54.9<sup>3</sup>
Matches 289, Conservative
                                                                                                                                 [1]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The deficition of a third distinct estrogen receptor and reclassification of estrogen receptors in telecosts.";

Teclassification of estrogen receptors in telecosts.";

Proc. Natl. Acad. Sci. U.S.A. 97:10751-10756(2000).

ER-ALPHA, AND ACTIVATES EXPRESSION OF REPORTER GENES CONTAINING ESTROGEN RESPONSE ELEMENTS (ERR) IN AN ESTROGEN-DEPENDENT MANNER.

C. I. SUBUNIT: BINDS DAR AS A HOMODIMER. CAN FORM A HETERODIMER WITH ER-CHORDINITY. BINDS DAR AS A HOMODIMER. CAN FORM A HETERODIMER WITH ER-CHORDINITY. BUNDANT IN THE LIVER AND TESTES, LESS ABUNDANT IN THE DOMAIN.

C. I. DOMAIN: Composed of three domains: a modulating N-terminal domain, a DNA-binding domain and a C-terminal steroid-binding domain.

SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
               SQEMKSVPCPLSGNEVVNMALTPEELIARIMDAEPPEIYLMXDMKKPFTEANVMMSLTNL 338
                                                 ADKELVHMISWAKKI PGFVELSLFDQVRLILESCWMEVLMMGLMWRSIDHPGKLIFAPDLV 361
                                                                            ADXBLVHMISWAKKVPGFVBLSLFDQVHLLRCCWLBVLMLGLMWRSVNHPGKLIFSPDLS 398
                                                                                                            421
                                                                                                                        -----ELLLDALSPEQLVLTLLEAEPPHV-LISRPSAPFTEASWMMSLTKL
                                                                                                            LDRDEGEKCVEGILE I PDMLLATTSRFRELKI QHKEYL CVKAMILLNSSMYPLVTATQDAD
                                                                                                                                                                  SSR---KLAHLINAVTDALVWVIAKSGISSQQQSMRLANLLMLLSHVRHASNKGMEHLLN
                                                                                                                                                                                  ELQRRSKILCLIDSVTDALVWAISKTGLSFQQRSTRLAHLILMLISHIRHLSNKGWDHIHC
                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Last sequence update)
18strogen receptor beta (ER-beta)
18strogen receptor beta (ER-beta)
18stropogonias undulatus (Atlantic croaker).
18ukaryota: Metazoa; Chordata; Cramiata; Vertebrata; Buteleostem;
18ctinopterygii; Neopterygii; Teleostei; Receleostei;
18ctinopterygii; Percomorpha; Perciformes; Percoidei;
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                                                                                                                                                                                                                                     MKCKNVVPVYDLLLEMINAHVIRGCKSSITGSECSPAEDSKSKEGS 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUB=Cvary;
MEDLINE=20461442; PubMed=11005855;
Hawkins M.B., Thornton J.W., Crews D., Skipper J.K., Dotte
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                                                                                                                                                                                                                                                                                                                        673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR000336; Hormone_rec_lig.
Interpro; IPR001723; Stdhrum_receptor.
Interpro; IPR008946; Str ncl_receptor.
Interpro; IPR001628; Znf_C4steroid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF298181; AAG16711.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00104; hormone_rec; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sciaenidae, Micropogonias.
NCBL_TaxID=29154;
                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              subfamily.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCEGCKAPFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLRKCYEVGMVKCGSRRERC 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198 SCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLRKCYBVGMMKCGVRRERC 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225 GYRLVRRORS------ADEQLHCAGKAKRSGGH------AP--RVRELLLLDALSP 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           444 SGISSQQQSMRLANILMILSHVRHASNKGMEHLLINMKCKNVVPVYDLLLLEMLNAHVLRGC 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRFRELKLOHKEYLCVKAMILLNSSMYPLVTAT-ODADSSRKLAHLLNAVTDALVWVIAK 443
                                                                                                                                                                                                                                                                                                                                                                                                                        84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266 EQLVLTLLBABPPHV-LISRPSAPFTEASMMASLTKLADKELVHMISWAKKIPGFVELSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 -SLEHTLPVNRETLKRKVSG-----NRCASPYTGPGSKRDAHFCAVCSDYASGYHYGVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPSSINSPSSYNCSQSILPLEHGSIYIPSSYVDSHHEY----PAMTFYSPAVMNYSIPSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 VIINLEGGPGR--QTISPNVLMPIPGH--LSPLVVHRQLSHLYARPQ-KSPWCEAR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 SPGLL--PAVYS---PPLGMDSHTVCIPSPYTDSSHEYNHSHGPLTFYSPSVLSYSRPP-
                                                                                                                                                                                                                                                                                                                                         62; Gaps
PRINTS; PRO0398; STROHORMONER.
PRINTS; PRO047; STROHORMONER.
PRODOM; PRO000039; Znf_C4steroid; 1.
SMART; SM00430; HOL1; 1.
SMART; SM00399; Znf_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
Receptor; Transcription regulation; DNA-binding; Nuclear protein; Zinc-finger; Steroid-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                 Length 673;
                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                       STEROID-BINDING.
28394517577B3D01 CRC64;
                                                                                                                                                         MODULATING.
NUCLEAR RECEPTOR-TYPE.
                                                                                                                                                                                                                                                                                                 51.0%; Score 1431; DB 1;
53.5%; Pred. No. 8.5e-106;
tive 76; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OFTES:
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FSE-2003 (Rel. 41, Last annotation update)
28-FSE-COGEN receptor beta (ER-beta) (Fragment).
ESR2 OR NR3A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             504 KSSITGSECSPAEDSKS-KEGSQNPQ 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----GSQPSSSPSSETYSDQHQYPQ 577
                                                                                                                                                                                                 C4-TYPE.
C4-TYPE.
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                                                                                                                                                                                                                                         653 S.
74680 MW;
                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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242
                                                                                                                                                                                                                                         248 6
673 AA;
                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                 / Match
Local Simi
hes 303;
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ZN FING
ZN FING
                                                                                                                                                                                                                                       DOMAIN
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MEDLINE-2013291; PubMed=10644527;
MEDLINE-2013291; PubMed=10644527;
MEDLINE-2013291; PubMed=10644527;
MEDLINE-2013291; PubMed=10644527;
MEDLINE-2013291; PubMed=10644527;
Mu X. H., Smith G.C.S., Nathanielsz P.W.;
Mu X. H., Smith G.C.S., Nathanielsz P.W.;
Mu X. H., Smith G.C.S., Nathanielsz P.W.;
Mu X. Prysiol. 278:C190-C198 (2000).
Mu J. Physiol. 278:C190-C198 (2000).
Mu J. Physi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDLVLDRDEGKCVEGILEIFDMLLATTSRFRELKLQHKEYLCVKAMILLNSSMYPLVTAT 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 QDADSSRKLAHILINAVTDALVWVIAKSGISSQQQSMRLANLIMLLSHVRHASNKGMBHLL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 LIKLADKELVHMISWAKKIPGFVELSLFDQVRLLESCWMBVLMMGLMWRSIDHPGKLIFA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QDADSSRKLAHLLNAVTDALVWVIAKSGISSQQQSMRLANLLMLLSHVRHASNKGMEHLL 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN: Composed of three domains: a modulating N-terminal domain, a DNA-binding domain and a C-terminal steroid-binding domain. SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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HSSP; P03372; IERR.
InterPro; IPR001723; Stdhrmn receptor.
InterPro; IPR001723; Stdhrmn receptor.
InterPro; IPR001846; Str_ncl_receptor.
InterPro; IPR001828; Znf_G4steroid.
Pfam: PF00104; hormone_receptor.
Pfam: PF00104; hormone_receptor.
PRINTS; PR001393; STREGENOMER.
SMART; SM00430; HOL1; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; PARTIAL.
Receptor; Transcription regulation; DNA-binding; Nuclear protein; Zinc-finger; Steroid-binding; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STEROID-BINDING.
PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49.8%; Score 1398; DB 1; Length 279; 98.2%; Pred. No. 1.1e-103; Live 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <1 >279 STEROID-BINDING.
251 251 PHOSPHORYLATION (BY SIMILA
279 279 AA; 31105 MW; 858D9B7D01DA0301 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 SMKCKNVVPVYDLLLEMLNAHVLRGCKSSITGSECSPAE 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NMKCKNVVPVYDLLLEMLNAHVLRGCKSSITGSECSPAE 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 98.2°
Matches 274; Conservative
Cercopithecinae; Macaca.
NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   >279
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Search completed: June 20, 2004, 10:37:40 Job time : 19 secs

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Q8BG65,
Q8BG65;
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Q95me9 callithrix
Q91286 mus musculu
Q96231 homo sapien
Q902e6 squalus aca
Q902e9 cyprimus ca
Q71232 brachydanic
Q90988 brachydanic
Q80462 brachydanic
Q8472 paralichthy
Q9047 acanthopagr
Q90499 brachydanic
Q90499 brachydanic
Q90499 canthopagr
Q90499 canthopagr
Q90499 canthopagr
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                                                                                                                                                                                                                                                                                     June 20, 2004, 10:34:32; Search time 46 Seconds (without alignments) 3635.318 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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QQ5MF0
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Q80ZEQ
Q8
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1: sp archea:*
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3: sp_bacteria:*
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sp_virus:*
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sp_unclassified:*
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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2805
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## ALIGNMENTS

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SEQUENCE FROM N.A.

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STRAIN=C57BL/61; TISSUB=Ovary;

The PANTOM Consortium,

The PANTOM Consortium,

The PANTOM Consortium,

The PANTOM Consortium,

The RIKEN Genome Exploration Research Group Phase I & II Team;

The Analysis of the mouse transcriptome based on functional annotation of moture 420.563-573 (2002).

Nature 420.563-573 (2002).

BMBL; AKOS4413; BAC35770.1; -...

PIR; PT0649; PT0712.

MGD; MGI:109392; BSC23770.1; -...

RGD; MG:0005496; F:steroid binding; IDA.

GO; GO:0007420; P:brain development; IMP.

GO; GO:0007420; P:brain development; IMP.

GO; GO:000552; P:regulation of transcription, DNA-dependent; IDA.

InterPro; IPR000546; Str nol receptor.

InterPro; IPR000546; Str nol receptor.

InterPro; IPR000468; Zur nol receptor.
                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                               Last sequence update)
Last annotation update)
567 AA
                                                                                    Created)
PRT;
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PRINTS; PR00047; STROIDFINGER.
ProDom; PD000035; Znf_C4steroid; 1.
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Pfam; PF00105; zf-C4; 1.
                                                01-MAR-2003 (TrEMBLrel. 2:
01-MAR-2003 (TrEMBLrel. 23
01-OCT-2003 (TrEMBLrel. 25
Estrogen receptor 2.
PRELIMINARY;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
Barrogen receptor beta 2.
Barrogen receptor beta 2.
Macaca arctoides (Stump-tailed macaque).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecidae; Macaca.
                                                                                                                                                                                                 18;
                                                                                                                                           DB 11; Length 567;
                                                                                                                                        88.5%; Score 2483; DB 11; Length 85.8%; Pred. No. 3.4e-219; ive 25; Mismatches 35; Indels
                                                            PTOR; 1.
BPB388C189FABE78 CRC64;
   SMART; SM00430; HOLI; 1.
SMART; SM00399; Znr C4; 1.
PROSTIE; PS00031; NUCLEAR RECEPTOR; SEQUENCE 567 AA; 63217 MW; BFB36
                                                                                                                                                                   Best Local Similarity 85.8 Matches 470; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 CASKAKRSGSHTPLVRELLLDALSPEQLVLTLLEAEPPHVLISRPSAPFTEASMWMSLTK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LADKELVHMISWAKKIPGFVELSLFDQVRLLESCWMEVLMMGLMWRSIDHPGKLIFAPDL 360
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
BOL-CCT-2003 (TrEMBLrel. 25, Last annotation update)
ERBETA2.
Callithrix jacchus (Common marmoset).
ENBATOGEN Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
NCBI_TAXID=9483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MDIXNSPSSINSPSSYNCSQSILPLEHGSIYIPSSYVDSHHBYPAMTFYSPAVMNYSIPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R GO; GO:0005634; C:nucleus; ISS.
R GO; GO:0002634; F:nestrogen receptor activity; ISS.
CG; GO:0048019; F:nestrogen receptor activity; ISS.
CG; GO:0048019; F:restrogen receptor signaling pathway; ISS.
CG; GO:0005496; F:steroid binding; ISS.
CG; GO:0005496; F:steroid binding; ISS.
CG; GO:0005496; F:steroid binding; ISS.
CG; GO:0005496; F:resquarive requiation of cell growth; ISS.
CG; GO:0006355; P:regulation of transcription, DNA-dependent; ISS.
CG; GO:0006355; P:regulation of transcription, DNA-dependent; ISS.
CG; GO:0006355; P:regulation of transcription, DNA-dependent; ISS.
CG; GO:0006356; P:regulation of transcription, DNA-dependent; ISS.
CG:00006356; P:regulation of transcription, DNA-dependent; ISS.
CG:00006356; P:regulation of transcription, DNA-dependent; ISS.
CG:00006356; P:regulation of transcription, DNA-dependent; ISS.
CG:00006365; P:regulation of transcription, DNA-depe
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PRINTS; PRO047; STROIDFINGER.
PROD00135; Znf_Casteroid; 1.
SWART; SMO0430; HOLI; 1.
SWART; SMO0399; ZnF_C4; 1.
PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
PROSITE; PS00031; NUCLEAR RECEPTOR; 2.
Transcription requalation; Znc; Znc-finger.
SEQUENCE 499 AA; 55782 MW; A91DA345C871BCOA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 86.3%; Score 2420; DB 6; Best Local Similarity 95.6%; Fred. No. 1.7e-213; Matches 456; Conservative 6; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ę
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RAY SEQUENCE FROM N.A.

RAY SEQUENCE FROM N.A.

RAY SCODIE G.A., Wilson J.A., Willar M.R., Macpherson S., Saunders P.T.;

RT "The estrogen receptor beta variant RRBete ox/ERBeta2 is expressed in RT a wide range of tissues in both Old and New World primates.";

RT a wide range of tissues in both Old and New World primates.";

RL SUBMILLIAR TOORNION NUCLEAR (BY SHALLARITY).

C. -: SIMELILLIAR LOCATION, NUCLEAR (BY SHALLARITY).

C. -: SIMELILLIAR LOCATION, NUCLEAR HORMONE RECEPTOR FAMILY.

DR GO; GO:0005707; Fisteroid hormone receptor activity; IEA.

GO; GO:000536; P:remscription factor activity; IEA.

GO; GO:0006356; P:remscription factor activity; IEA.

GO; GO:0006356; P:remscription factor activity; IEA.

GO; GO:0006356; P:remscription; IEA.

DR GO; GO:0006356; P:remscription; IEA.

GO; GO:0006356; P:remscription; IEA.

DR GO; GO:0006356; P:remscription; IEA.

DR FORDON POSSO STRUMPLE CEC 13.

B. InterPro; IPR00155; ELC4; I.

DR PERM; PR00165; Zrf C4steroid; I.

PR PRINTS; PR00105; Zrf C4steroid; I.

BR PRANTS; PR00105; Zrf C4steroid; I.

BR PRANTS; PR00105; Zrf C4steroid; I.

BR PRANTS; SW00439; Zrf C4; I.

DR ROSSITE; PS00011; NUCLEAR RECEPTOR; I.

BR PRANTS; SW00439; Zrf C4steroid; I.

BR PRANTS; SW00430; HOLI; I.

BR PRANTS; PR00105; Zrf C4steroid; I.

RYART; SW0039; Zrf C4; I.

BR PRANTS; SW00430; HOLI; I.

BR PRANTS; SW00430; HOLI; I.

BR PRANTS; SW00430; HOLI; I.

BR PRANTS; RYARTS; PR00105; Zrf C4steroid; I.

RYARTS; SW00430; HOLI; I.

BR PRANTS; RYARTS; PR00105; Zrf C4steroid; I.

RYARTS; SW00430; HOLI; I.

BR PRANTS; RYARTS; PR00105; Zrf C4steroid; I.

RYARTS; SW00430; HOLI; I.

BR PRANTS; RYARTS; RYARTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGKAKRSCGHAPRVREILILDALSPBOLVLTILEAEPPHVLISRPSAPPTEASMMSLTK 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NVINLEGGEGGRANTISPNVLWPTPGHLSPLVVHRQLSHLYAEPQKSPWCEARSLEHTLPVN 120
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des 434; Conservative
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ID 09
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DT 01
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75:76:TT 07 unc un

Created) Last sequence update) 203

(TrEMBLrel 19, (TrEMBLrel 19,

Q91286; 01-DEC-2001 01-DEC-2001

PRELIMINARY;

982160

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NEW STRAINFLURY;

Dang Z., van Bezooijen R., Karperien M., Papapoulos S., Lowik C.;

RT "Exposure of KS483 cells to estrogen enhances osteogenesis and inhibits adipogenesis."

RT 'Inhibits adipogenesis."

C. -: SURCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

C. -: SURCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

C. -: SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR PAMILY.

REME; ANOS4413; AAL15175.1; -.

DR GO; GO:0005496; F: steroid binding; IDA.

GO; GO:0006328; P: resqualtion of transcription, DNA-dependent; IDA.

DR GO; GO:0006329; P: regularion of transcription, DNA-dependent; IDA.

GO; GO:0006326; Hormone rec 119.

DR GO; GO:0006356; Hormone rec 119.

RIGHTP: IPRO010546; Str nol_receptor.

DR Fam; PRO0105; Are C45teroid.

Pfam; PRO0105; LAC4; I.

DR PRINTS; PRO0105; ZAF C4; I.

DR PRINTS; PRO0105; ZAF C4; I.

DR SWART; SM00399; ZAP C4; I.

DR PROSITER; PRO0105; ZAP C4; I.

DR PROD105; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SAPPTEASMAMSLIXLADKELVHMISWAKKIPGFVELSLFDQVRLLESCWMEVLAMGLAM 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RSIDHPGKLIFAPDLVLD-------RDEGKCVEGILEIFDWLLATTSRF 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106 PWCEARSLEHTLPVNRETLKRKVSGNRCASPVTGPGSKRDAFFCAVCSDYASGYHYGVWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 PWCEARSLEHTIPVNRETIKRKIGGSGCASPVTSPSAKRDAHFCAVCSDYASGYHYGVWS
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                                                                 Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
VCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
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Best Local Similarity 85.7%; Pred. No. 5.7e-200;
Matches 431; Conservative 22; Mismatches 32; Indels
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Estrogen receptor beta type II splice variant.
                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                      STRAIN=DDY;
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241 CAGKAKRSGGHAPRVRELLLDALSPEQLVLTLLEAEPPHVLISRPSAPFTEASWAMSLTK 300 NVTINLEGGPGRQTTSPNVLWPTPGHLSPLVVHRQLSHLYAEPQKSPWCBARSLEHTLPVN 120 NDYICPATNQCTIDKNRRKSCQACRLRKCYEVGMVKCGSRRERCGYRLVRRQRSADEQLH 240 9 1 MDIKNSPSSLNSPSSYNCSQSILPLEHGSIXIPSSYVDSHHEYPAMTFYSPAVMYYSIPS TISSUENCE FROM N.A.

C TISSUB-Testis,
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
Li Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, BC034181, AM424181.1; -..
GO; GO:0003700; Firanscription factor activity; IEA.
GO; GO:0003700; Firanscription factor activity; IEA.
GO; GO:0003755; Piranscription factor activity; IEA.
RO; GO:0006355; Piranscription factor activity; IEA.
RO; GO:000635; Firanscription factor activity; IEA.
InterPro; IPR001628; Znf_C4sferoid.
R Pfam; PR00047; STROIDFINGER.
R PRODOM; PR00035; Znf_C4steroid; 1.
R PRAMTS; RM00099; Znf_C4steroid; 1.
R PROSITE; PS00031; NUCLEAR_RECEPFOR; 1. 1 MDIKONSPSSLNSPSSYNCSQSILPLEHGSIY1PSSYVDSHHEYPAMTFYSPAVMOYSIPS RETLIKRKVSGNRCASPVTGPGSKRDAHFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGH 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical 35.9 Kps protein.
Homo sapiens (Human).
Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. Length 323; Indels l protein. 323 AA; 35944 MW; 158D376C56D3CA12 CRC64; Last sequence update) Last annotation update) 61.4%; Score 1723; DB 4; L 100.0%; Pred, No. 1.1e-149; ive 0; Mismatches 0; 323 AA 530 SGSECCSTEDSKSKEGSQNLQSQ 503 Created) TGSECSPAEDSKSKEGSQNPQSQ LADKELVHMISWAKKIPG 318 (TrEMBLrel. 19, 1 (TrEMBLrel. 19, 1 (TrEMBLrel. 25, 1 Best Local Similarity 100. Matches 318; Conservative PRELIMINARY; PRELIMINARY; 0902E6 0902E6; 01-DEC-2001 01-DEC-2001 01-OCT-2003 508 481 SEQUENCE 61 61 121 121 181 181 301 301 Query Match ઠ 셤 g ò Ω̈́ a ò å d ð ò ò

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NVTNLEGGPGROTTSPNVLWPTPGHLSPLVVHROLSHLYAEPOKSPWCEARSLEHTLPVN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 NDYICPATNOCTIDKORRKKSCOACRLRKCYEVGWVKCGSRRERCGYRLVRRQRSADEQLH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TKLADKELVHMISWAKKIPGFVELSLFDQVRLLESCWMEVLMMGLMWRSIDHPGKLIFAP 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83
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Priam; PF001105; zf-C4; 1.
PRINTS; PR00105; zf-C4; 1.
PRINTS; PR00047; STRDFNCMORE.
Probom; PD000035; znf_C4steroid; 1.
SMART; SM00430; hOLT: 1.
SMART; SM00430; hOLT: 1.
PROSITE; PS00031; NÜCLEAR_RECEPTOR; 1.
PROSITE; PS00031; NÜCLEAR_RECEPTOR; 1.
PROSITE; PS00031; Zinc: Zinc: Zinc-finger.
STRANSCRIPTION; Zinc: Zinc-finger.
SEQUENCE 542 AA; 61285 MW; D539A29A9718DD37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 IKNSPTGLTTQPQYS---STLPGLSEHGPVCIPSSYVENRHEFPTLAFYSPSILGYSMPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNLADRELVHMIAWAKKVPGFVELDLHDQVQLLECCWLEVLMVGLMWRSIEYPGKLLFAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 DASGPDGTIVRQSLSPSMYWSSTGHVSPITLHCQQPIMYARPPKSPWDDLRSGDQHL-LN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 CAGKAKRSG-GHAPRVRELLLDALSPEQLVLTLLEARPPHVL-ISRPSAPFTEASMYMSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 IXNSPSSINSPSSYNCSOSILP--LEHGSIYIPSSYVDSHHEYPAMTFYSFAVMNYSIPS
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                                   Chondrichthyes;
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              Squalus acanthias (Spiny dogfish).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Chor
Blasmobranchii, Squalea, Squaloidei, Squalidae, Squalus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 60.3%; Score 1691; DB 13; Best Local Similarity 61.7%; Pred. No. 1.9e-146; Matches 320; Conservative 83; Mismatches 98;
receptor beta.
                                                                              NCBI_TaxID=7797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 IPGEVELSLIDQVRLILBSCWMEVIAVGLAWRSIDHPGRLIFAPDLVLDRDEGKCVBGILE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             376 IFDMLLATTSRFRELKLOHKBYLCVKAMILLNSSMYPLVTATQDADSSRKLAHLLNAVTD 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPGFVELSLFDQVRLLESCWMEVLAMGLAMWRSIDHPGKLIFAPDLVLDRDEGKCVEGILE 375
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A Zhang X., Harris H.;
A Zhang X., Harris H.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
B. Submitted (OCT-2002) Firsterial hormone receptor (OCT-2002) to the EMBL/GenBank/DDBJ dependent; IEA.
B. InterPro; IPR001923; Stdhrm receptor (OCT-2002) to the EMBL/GenBank/DDBJ databases.
B. InterPro; IPR001928; Zhf_GenBank/DDBJ databases.
B. InterPro; IPR00104; hormone received (OCT-2002) to the EMBL/GenBank/DDBJ databases.
B. PEGRIF (OCT-2002) to the EMBL/GenBank/DDBJ databases.
B. PEGRIF (OCT-2002) to the EMBL/GenBank/DDBJ databases.
B. Submitted (OCT-2002) to the EMBL/
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                                                                                                                                                                                                                                                                                                                                                               ESR2.
Cavia porcellus (Guinea pig).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Hystricognathi; Caviidae; Cavia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON TER 1 1 1
SEQUENCE 335 AA; 37779 MW; P8B0144F33EA7AB0 CRC64;
                              501 MKCKGNVVPFYDLLLEMLDAHVIY-----SRTKPSDD 531
                                                                                                                                                                                                                                                01-WAR-2003 (TrEMBLrel. 23, Created)
1-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Estrogen receptor 2 (Pragment).
   MKCKNVVPVYDLLLEMINAHVIRGCKSSITGSECSPAED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00398; STRDHORMONER
                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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   479
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Q8JJB9
ID Q8JJJ
                                                                                                                                       RESULT 7
08CGK9
1D 08CG
AC 08CG
AC 08CG
DT 01-M
DT 01-
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WATABOR S., Matsumoto T., Kobayashi M.;

Watabe S., Matsumoto T., Kobayashi M.;

"Common carp mRNA for estrogen receptor beta, complete cds.";

SIMILARITY.

"Common carp mRNA for estrogen receptor beta, complete cds.";

"Common carp mRNA for estrogen receptor databases."

"I SINCELLULAR LOCATION; NUCLEAR HORMONE RECEPTOR FAMILY.

"ENTILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.

"ENTILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.

"GO, GO:0005300; F:transcription factor activity; IEA.

"GO, GO:0005300; F:transcription factor activity; IEA.

"GO, GO:0005350; P:transcription factor activity; IEA.

"GO, GO:0005350; P:transcription; IEA.

"INTER-PRO; IPR001523; Etchnum. receptor.

"INTER-PRO; IPR001523; Etchnum. receptor.

"INTER-PRO; IPR001524; Str. ncl. receptor.

"INTER-PRO; IPR001628; Znf. C45eroid.

"PRINTS; PR00196; STRDHORNONER.

"PRINTS; PR00047; STRDHORNONER.

"PRINTS; PR00047; STRDHORNONER.

"PROSTE; PS00031; NUCLEAR RECEPTOR; 1.

"PROSTED: PS00031; NUCLEAR RECEPTOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 ROTTSPNVLWPTPGHLSPLVVHRQLSHLYA-EPQKSPWCEARSLEHTLPVNRETL-KRKV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189 NOCTIDKNRRKSCOACKLRKCYBVGMVKCGSRRERCGYRLVRRQRSADEQ--LHCAGKAK 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200 NQCTIDKNRRKSCQACRLRKCYEVGAMAKCGLRRDRGSY----QQRGARQKRLARRSGRAMR 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256 TCGPRSQEIKSVPRPLGGNKVVSIALSPEELIARIMDABPPEIYLANDVKKPFTBANIMM 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         316 SLTNLADKELVHAISWAKKIPGFVELSLPDQVHLLECCWLBVLALGLAMRSVNHPGKLIF 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       297 SLIKLADKELVHMISWAKKIPGFVELSLFDQVRLLESCHMEVLMMGLMWRSIDHPGKLIF 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     357 APDLVLDRDEGKCVEGILEIFDWLLATTSRFRELKLQHKEYLCVKAMILLNSSM-YPLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 RSGGHAPRVR-----ELLIDALSPEQLVLTLLEAEPPHV-LISRPSAPFTEASMOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 SPSSYNCSQSILPLEHGSIYIPSSYVDSHHEYPAMTFYSPAVMNYSIPSNYTNLEGGPG-
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
BStrogen receptor beta.
Cyprinus carpio (Common carp).
Butaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes, Cyprinides, Cyprinus.
NCBI_TaxID=7962;
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Best Local Similarity 55.4%; Pred. No. 2.9e-126;
Matches 297; Conservative 80; Mismatches 130; Indels
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251

301 319 361

204 DKNRRKSCQACRIERKCYEVGAMAKCGIRRDRSSY----QQRGAQQKRLVRFSGRNRMTGPR 259

DKNRRKSCQACRLRKCYBVGWVKCGSRRERCGYRLVRRQRSADBQ--LHCAGKAKRSGGH

194

146 TS--VSLRGKADMHYCAVCSDYASGYHYGVWSCBGCKAFFKRSIQGHNDYICPATNQCTI

134 ASPVTGPGSKRDAHFCAVCSDYASGYHYGVWSCBGCKAFFKRSIQGHNDYICPATNOCTI

74 TSPNVLMPTPGHLSPLVVHRQLSHLYABPQKSPWCEARSLEHTLPVNRETLKRKVSGNRC 133

| : | : | : | : | : | | : | 86 LSPTLFWPPHSHVSSLTLQQQSRLQQNHATSGTWTEHTPHDHVBEENSKPLVKRVADTEE

85

362

302 ADKELVHMISWAKKIPGFVELSLFDQVRLLESCHWEVLMMGIMWRSIDHPGKLIFAPDLV

260 SQEIKSIPRPLSGNEVVRISLSPEELISRIMEABPPEIYLMKDPYRANVMMSLTNL

252 APRVR------RULLDALSPEQLVLTLLEAEPPHV-LISRPSAPFTEASMMMSLTKL

499

421 DSSRKLAHLLMAVTDALVWVIAKSGISSOOOSMRLANLLMLLSHVRHASNKGMEHLLMMK 480

481 CKNVVPVYDLLLEMLNAHVLRGCKSSITGSECSPA-EDSKS 520 

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SQUENCE FROM N.A.

STRAIN-AB; TISSUE-Body;

Strain-AB; TISSUE-Body;

Strain-AB; TISSUE-Body;

Strain-AB; TISSUE-Body;

Strain-AB; TISSUE-Body;

Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; BC044349; AM44349.1; -.

EMBL; BC04349; AM44349.1; -.

GO; GO:0003707; F:steroid hormone receptor activity; IEA.

GO; GO:0003700; F:regulation of transcription, DNA-dependent; IEA.

EQ; GO:0003707; F:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR001628; Bornone_rec_lig.

InterPro; IPR001628; Strindl_receptor.

InterPro; IPR001658; Strindl_receptor.

InterPro; IPR001658; Strindl_receptor.

InterPro; IPR00105; zf-C4; I.

Fram; PR00105; zf-C4; I.

Fram; PR00105; zf-C4; I.

Fram; PR00105; zf-C4; I.

Fram; PR00105; zf-C4; I.

Franscription, DNA-dependent; ISA

SMART; SM00399; Znf C4steroid; I.

SMART; SM00399; Znf C4steroid; I.

SMART; SM00399; Znf C4; I.

FROSITE; PR00399; Znf C4; I.

FROSITE; PR00318; NUCLEAR RREEPTOR; I.

SEQUENCE SS3 AA; G2339 MW; IB7E78AB66AD7AS3 CRC64;
                                                                                                                                                                                                                                                       01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
EST2 protein.
EST2 protein.
Exachydanio rerio (Zebrafish) (Danio rerio).
Enkaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
NUSI_TAXID=7955;
                                                476 LENWIKCKONTVPVYDLLLEMINAHVIRGCKSSITGSECSPA-EDSKSKEGSQNPQSQ
                                                                            496 IHCMCMKWKWYDLYDLILLEMLDAHIMHSSRLSHSGPRAAPAPKESKGVQBALTRTSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.9%; Score 1455.5; DB 13; Length 553;
55.7%; Pred. No. 8.3e-125;
tive 78; Mismatches 126; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
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Best Local Similarity 55.73
Matches 290; Conservative
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxIb=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

Menuet A., Pellegrini E., Anglade I., Blaise O., Laudet V., Kah O.,

Pakdel F.,

"Binding characteristics, transactivation properties and central
                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                           Brachydanio rerio (Zebrafish) (Danio rerio)
                                                                                                                                            Created)
                                                                  PRT;
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Pfam; PF00105; zf-C4; 1.
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PRINTS; PR00047; STROIDFINGER
                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-OCT-2003 (TrEMBLrel. 25,
                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                         ZfER-beta2 protein.
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RESULT 10
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9

Gaps

Gaps

73 85

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us-08-906-365-2.rspt

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252 APRVREL-----LIDALSPEQLVLTILEAEPPHV-LISRESAPFTEASWAMSLIKL 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      320 ADKELVHMISWAKKIPGFVELSLFDQVHLLECCWLEVLMLGLMWRSVNHPGKLIFSPDLC 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421 DSSRKLAHLINAVTDALVWVIAKSGISSQQQSMRLANLLMILSHVRHASNKGMEHLLNMK 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 ISPNVLMPTPGHLSPLVVHRQLSHLYAEPQKSPWCEARSLEHTLPVNRETLKRKVSGNRC 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194 DYNRRKSCQACRLRKCYEVGMYKCGSRRERCGYRLVRRQRSADEQ--LHCAGKAKRSGGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146 TS--VSLRGKADMHYCAVCSDYASGYHYGVWSCBGCKAFFKRSIQGHNDYICPATNQCTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 DKNRRKSCOACKLRKCYEVGMMKCGLRADRSSY----QRGAQQKRLVRFSGRMRMTGPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260 SQEIKSIPRPLSGNEGARISLSPEELISRIMEAEPPEIYLMKDMKKPFTEANVMMSLTNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 YNCSQSILPLEHGSIYIPSSYVDSHHEYPAMTFYSPAVMNYSIP--SNVTNLEGGPGRQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 362 LDRDEGKCVEGILEIFDMLLATTSRFRELKLOHKEYLCVKAMILLNSSM-YPLVTATODA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 PNSSSPSILPVENHPICIPSPYTDLGHDFSTLPFYSPALLGYSTSPLSDCSSV-----RQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 ASPVTGPGSKRDAHFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes; Pleuronectoidei; Paralichthyidae; Paralichthys.

NCBI_TaxID=8255;
[1]
Piregulation of transcription, DNA-dependent; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                  13; Length 553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27;
                                                                                                                                                                                                                                                                                                                                                                                                               51.4%; Score 1441.5; DB 13; Lengt
55.3%; Pred. No. 1.6e-123;
.ive 76; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              520
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                                                                                                                                                                                                                                                                                                                                                                   62196 MW; 928FC9E0D339844B CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              481 CKNVVPVYDLLLEMLNAHVLRGCKSSITGSECSPA-BDSKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IRR00536; Hormone rec lig.
InterPro; IRR00536; Hormone rec lig.
InterPro; IRR00846; Str ncl receptor.
InterPro; IRR00846; Str ncl receptor.
InterPro; IRR00846; Str ncl receptor.
InterPro; IRR001629; Znf_C4steroid.
Pfam; PP00104; hormone rec; 1.
Pfam; PP00105; zf-C4; I.
Prants; PR00195; Zf-C4; I.
PRINTS; PR00195; Zf-C4; I.
ProDom; PD000035; Znf_C4steroid; I.
SWART; SW00430; HOLI; I.
SWART; SW00399; Znf_C4; I.
PROSITE; PS00031; NUCLEAR_RECEPTOR; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 55.3
nes 288; Conservative
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ERB.
                                                                                                                                                                                                                                                                                                                                                                        553 AA;
           GO: 0006355;
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                                                                                                                                                                                                                                                                                                                                                                                                                          74 TSPNVLWPTPCHLSPLVVHROLSHLYAEPOKSPWCBARSLEHTLPVNRETLKRKVSGNRC 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SQIKSIPRPLSGNEVVRISLSPBEBLISRIMEABPPBIYLMKDMKKPFTEANVMMSLTNL
                                                                                                                                                                                                                                                                                                                                                        APRVR------ELLLDALSPEQLVLTLLEAEPPHV-LISRPSAPFTEASWMMSLTKL
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                                                                                                                                                                                                                                                                                                                            YNCSOSILPLEHGSIYIPSSYVDSHHEYPAMTFYSPAVMNYSIP--SNVTNLEGGPGRQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 ASPVTGPGSKRDAHFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCTI
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     ProDom; PD000035; Znf_C4steroid; 1.
SWART; SM00430; HCLI; 1.
PROSITE; SM00399; ZnF_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription, Transcription regulation; Zinc, Zinc, Einger.
SEQUENCE 553 AA, 62323 MM; 84C4DE6C7AC0C5ED CRC64;
                                                                                                                                                                                                                                                                     Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.

NCBL TaxID=7955;
                                                                                                                                                                                                                                                                  27;
                                                                                                                                                                                                                    DB 13, Length 553
                                                                                                                                                                                                              Match 51.9%; Score 1454.5; DB 13, Length Local Similarity 55.7%; Pred. No. 1e-124; les 290; Conservative 78; Mismatches 126; Indels
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GO; GO:0005634; F:steroid hormone receptor activity; IEA.
GO; GO:0003700; F:steroid hormone receptor activity; IEA.
GO; GO:0003700; P:transcription factor activity; IEA.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Bstrogen receptor beta a.
Brachydanio rerio (Zebrafish) (Danio rerio).
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MEDLINE=22347324; PubMed=12459262;
Lassiter C.S., Kelley B., Linney E.;
"Genomic Structure and Embryonic Expression at (ERbeta a) in Zebrafish (Danio rerio).";
Gene 299:141-151(2002).
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REQUENCE FROW N.A.

Kitano T., Sakimara N., Takamune K., Nagahama Y., Abe S.,

Kitano T., Sakimara N., Takamune K., Nagahama Y., Abe S.,

"Role of estrogen receptor in gonadal sex differentiation in Japanese
flounder (Paralichthys olivaceus) ";

"Bole of estrogen receptor in gonadal sex differentiation in Japanese
c. = Submitted (And-2001) to the EMBL/GenBank/DbbJ databases.

"Role of Condomination of The EMBL/GenBank/DbbJ databases.
"Role of Condomination of The NUCLEAR HORWONE RECEPTOR FAMILY.

EMBL; ABO70530; BAB85623.1; -

"ROLE OF CONDOMINATION OF THE NUCLEAR HORWONE RECEPTOR FAMILY.

EMBL; ABO70530; BAB85623.1; -

ROLE OF CONDOMINATION OF THE NUCLEAR HORWONE RECEPTOR FAMILY.

EMBL; ABO70530; Farth binding; IEA.

GO; GO:0005524; First binding; IEA.

GO; GO:0005524; First binding; IEA.

GO; GO:0005524; First binding; IEA.

GO; GO:0005525; First binding; IEA.

GO; GO:0005525; First binding; IEA.

GO; GO:0005525; First binding; IEA.

GO; GO:0006350; First binding; IEA.

InterPro; IPRO0152; First binding; IEA.

REALY: ROUGHY; STRODIPENDER.

PRODITE; ROUGHY; STRODIPENDER.

PRODITE; ROUGHY; STRODIPENDER.

PRODITE; ROUGHY; STRODIPENDER.

PROSITE; PRO0190; CYTCCHEOME C. 1.

ROMART; SMO0399; CATPORENDER.

PROSITE; PRO01915; ATRODIPENDER.

PROSITE; PRO01915; ATRODIPENDER.

PROSITE; PRO0190; CYTCCHEOME C. 1.

PROFILE FOR COLOR FERSIBLIANE C. 
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Best Local Similarity 54.5%; Pred. No. 1.2e-120;
Matches 291; Conservative 66; Mismatches 146; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Huang Y.-S., Yueh W.-S., Huang J.-D., Du J.-L., Sun L.-T.,
Nagahama Y., Chang C.-F.;
"Cloning and Expression of Estrogen Receptors in the Protandrous Black
Poray (Acanthopagrus schlegeli): Implication of Sex Change
Mechanism.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mernaniam.";

Mar. Biotechnol. 4:236-246(2002).

Rami. Av074779; AaL82742.1;

BMG, GO:0005649; F:ATP binding; IEA.

GO; GO:0005549; F:ATP binding; IEA.

GO; GO:0003709; F:seteroid hormone receptor activity; IEA.

GO; GO:0003700; F:seteroid hormone receptor activity; IEA.

GO; GO:0003700; F:seteroid hormone receptor activity; IEA.

GO; GO:0001892; P:Percon transport; IEA.

GO; GO:000535; P:regulation of transcription, DNA-dependent; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

GO; GO:0005355; P:regulation of transcription, DNA-dependent; IEA.

GO; GO:0005355; F:REGULATION of transcription, DNA-dependent; IEA.

InterPro; IPR001723; Stdhrmn_receptor.

BR Fam; PF00104; hormone rec; 1.

SRAMXT; SR00439; STRCDHORNONER.

PROSITE; PR00139; ATREDGRANURE.

BROSITE; PS000131; NUCLEAR_REGEPTOR; 1.

PROSITE; PS00031; NUCLEAR_REGEPTOR; 1.
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                                                                                                                                                                                                                                                                                                                                                                                     Estrogen receptor beta.

Acanthopagrus schlegeli (Black porgy).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;

NCBI TaxID=72011;
481 CKNVVPVYDLLLEMLNAHVLRGCK-----SSITGSBCSPAEDSKSKEGSON
                                    498 MKNMVDLYDELLEMIDAHIMHSSRIPHHASPQPEFTDQGEVPARPGSSGNGSSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 13; Length 553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.2%; Score 1409.5; DB 13; Lengt
52.9%; Pred. No. 1.4e-120;
tive 71; Mismatches 133; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         553 AA; 61953 MW; 7CC094638CEE4AA2 CRC64;
                                                                                                                                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                              Ā
                                                                                                                                                                                                                                              553
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Best Local Similarity 52.9%
Matches 286; Conservative
                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. TISSUE=Ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Receptor.
SEQUENCE
                                                                                                                                                                            RESULT 13
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                                                                                                                                                                                                                                                                                  SOW REPRESENTATION OF THE PROPERTY AND THE PROPERTY OF THE PRO
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GEVELSLEDQVRLLESCWMEVLMMGLMWRSIDHPGKLIFAPDLVLDRDEGKCVEGILEIF 377
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RA PANCEL R., PELIGGINI E., Anglade I., Blaise O., Laudet V., Kah O., RA Pakdel F.;

Pakdel F.;

Pakdel F.;

Pakdel F.;

Pakdel F.;

Patholing characteristics, transactivation properties and central strength of three estrogen receptor subtypes in zebrafish.";

Submitted (SEP-201) to the EMBL/GenBank/DDBJ databases.

C. :- SIMILARITY: BLONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.

EMBL; AJ414566; CAC93848.1; -.

DR GO: 00001707; Piederron transporter activity; IEA.

GO: 00001707; Piederron transporter activity; IEA.

GO: 00001707; Piederron transport activity; IEA.

GO: 0000189; Piederron transport; IEA.

GO: 0000189; Piederron transport; IEA.

GO: 0000189; Piederron transport activity; IEA.

GO: 0000189; Piederron transport; IEA.

GO: 0000189; Piederron transport; IEA.

GO: 0000189; Piederron transcription, DNA-dependent; IEA.

GO: 0000189; Stranscription; IEA.

InterPro; IPR00036; Hormone_rec_lig.

InterPro; IPR001628; Stf.—C4sTeroid.

BRINTS: PR00105; zf-C4; I.

PEAM; PF00106; zf-C4; I.

PRINTS: PR00047; STROIDFINGER.

DR START; SM00430; HOLI: 1.
                                                                                                                                        437 LVWVIAKSGISSQQQSMRLANLIMLLSHVRHASNKGWEHILINMKCKNVVPVYDLLLEMLN
                                                                                                                                                                                                                                                                                                                                                                                                                   430 DMLLAATSRFRELKLQREBYVCLKAMILLNSNLCSSSPQTBEELESRNKLKRLDSVIDA
                 --- APRVREL
                                                                                                             259 LLDALSPEQIVITILEAEPPHV-LISRPSAPFTEASWAMSLTKLADKELVHMISWAKKIP
                                                                                                                                                                                                                                                                                                378 DMLLATTSRFRELKLQHKEYLCVKAMILLNSSMYPLVTAT-QDADSSRKLAHLLNAVTDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMBRT; SW00399; ZNP_C4; 1.
PROSITE; PS00190; CYTOCHROME C; 1.
PROSITE; PS00031; NUCLEAR ENCEPTOR; 1.
DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZERR-betal protein.
ZERR-BETAL.
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Moopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                      ---ADEQLHCAGKAKRSGGH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 497 AHVLRGCKSSITGSECSPAEDSKSKEGSQNPQ
                      GSRRERCGYRLVRRQRS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-OCT-2003 (TrEMBLrel. 25,
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                      238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  473 MEHILMNKCKNVVPVYYDLILEMINAHVL-----RGCKSSITGSECSPAEDSKSKEGSON 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 NVTNLEG--GPGRQTTSPNVLWPTPGHLSPLVVHRQL-----SHLYARPQKSPWC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLRKCYEVGMVKC 217
                                                                                            293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSPGLL--PAVYSPRQG---MDSHTVYIPSPYTDNNQBYNHGSGSVSFYSPSVLSYARPS
                                                                                                                    ijpapdividrdegekcvegileipdmilattsrpreikiqhkevlcvkamilinssm-vp
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|ijpspolsisrebgscvqqfleipdmilaatsrvreikiqresvvcikamilinsnmcls
                                                                                                                                                                                                                                                                                                                                                                                                    294 NPMSLIXIADKELVHMISWAKKIPGFVELSLFDQVRILBSCWMEVLMMGLMWRSIDHPGK
                                                                                                                                                                                                                                                                                                                                                                           LVTATQDADSSRXLAHLLNAVTDALVWVIAKSGISSQQQSMRLANLIMLISHVRHASNKG
                                                                                            OLHCAGKAKRSGGHAPRVRELLL - - DALSPEQLVITLLBAEPPHV - LISRPSAPFTEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Perciformes, Labroidei,
Labridae, Halichoeres.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                subtypes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Park J.-G., Kim S.-J.,
"Molecular cloning and expression of two estrogen receptor protogynous wrasse, Halichoeres tenuispinis.";
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY305027; AAP72179.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cch 49.9%; Score 1401; DB 13; al Similarity 52.4%; Pred. No. 1.1e-119; 300; Conservative 73; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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Best Local Similarity
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TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   527 P 527
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177 YGVWSCEGCKAFPKRSIQGHNDYICPATNQCTIDKSRRKSCQACRLRKCYBVGMMKGGVR 236
                                                                                                                                                                                                                                                                                               -- AVMAYSIPSNVTNLEGGPGRQTTSPNVLWPTPGHL---SPLVVHRQLSHLYABPQKSP 106
                                                                                                                                   WVIAKSGISSQQQSMRLANLLMLLSHVRHASNKGMEHILLNMKCKNVVPVYDILLEMLNAH 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                RERCGYRLVRROR----SADEQLHCAGKAKR------SGGHAPRVRELLL 260
                                                                                                                                                                                                                                                                      11 NSPSSYNCSOSILP-----LEHGSIYIPSSYVDSHHEYP------AMTRYSP- 51
                                                     81; Gaps
                             Query Match
49.8%; Score 1397.5; DB 13; Length 592;
Best Local Similarity 51.6%; Pred. No. 1.9e-119;
Matches 300; Conservative 79; Mismatches 121; Indels 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             499 VLRGCK-----SSITGSBCSPARDSKSKEGSQNPQSQ 530
Transcription regulation; Zinc, Zinc-finger.
SEQUENCE 592 AA; 66046 MW; 7F65218E2C03F1B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   533 ASOSSEMLEDROOSPENLHTSRPOPDLKDSDOETPHSPRAR 573
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Search completed: June 20, 2004, 10:38:38 Job time : 48 secs

Sequence 3, Appli Sequence 1, Appli Sequence 9, Appli Sequence 6, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 19, Appli Sequence 19, Appli Sequence 18, Appli Sequence 7, Appli Sequence 6, Appli

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121 RETLKRKVSGNRCASPVTGPGSKRDAHFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGH 180
121 RETLKRKVSGNRCASPVTGPGSKRDAHFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGH 180
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Best Local Similarity 100.0%; Score 2805; DB 4; Length 530;
Best Local Similarity 100.0%; Pred. No. 1.4e-291;
Matches 530; Conservative 0; Mismatches 0; Indels 0
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US-U9-500-088-25

Patent No. 6680368

GENERAL INPORMATION:
TITLE OF INVESTION:
FILE REFERENCE: 0/96193 G81

CURRENT APPLICATION: NO. 66803681 Estrogen Receptor
TITLE OF INVESTION: NO. 66803681 Estrogen Receptor
CURRENT PILING DATE: U8/09/608,088

CURRENT PILING DATE: 1090-06-30

PRIOR APPLICATION NUMBER: U8/09/608,088

CURRENT PILING DATE: 1990-03-26

PRIOR PILING DATE: 1996-01-22

PRIOR PILING DATE: 1996-03-26

NUMBER: OF SEQ ID NOS: 28

SOFTWARE: Patentin version 3.0

SEQ ID NO 25

LENOTH: 530

TYPE: PRT

COGANISM: Homo sapiens
US-09-608-088-25
US-08-693-940-3

US-09-566-660-3

US-08-836-620A-9

US-08-836-620A-10

US-08-836-620A-10

US-08-836-620A-10

US-09-141-000-2

US-09-141-000-2

US-09-141-000-2

US-08-836-620A-19

US-08-836-620A-19

US-09-141-000-6

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US-09-155-800-7
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                                                                                                                                                             June 20, 2004, 10:36:03; Search time 23 Seconds (without alignments) 1189.642 Million cell updates/sec
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1 MDIKNSPSBINGPSSYNCSQ......ECSPAEDSKSKEGSQNPQSQ 530
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1: /cgrl2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgrl2_6/ptodata/2/iaa/5B_COMB.pep:*
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5: /cgrl2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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                               GenCore version 5.1,6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-561-711-1
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US-09-561-711-1
US-08-836-620A-3
US-08-836-620A-13
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RESULT 4
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                                       DSSRKIAHLINAVTDALVWVIAKSGISSQQOSMRLANLLMLLSHVRHASNKGMEHLINMK 480
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78
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19 NVTNLEGGPGRQTTSPNVLWPTPGHLSPLVVHRQLSHLYAEPOXSPWCEARSLEHTLFVN
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                                                                                                                                                                                                                                                                                  ; CHURLANT; MILKINSON, HILARY
; TITLE OF INVENTION: ESTROGEN RECEPTOR
; FILE REPERRENES: 20047Y
; CURRENT APPLICATION NUMBER: US/09/139,617
; CURRENT FILING DATE: 1998-08-25
; BARLIER APPLICATION NUMBER: 60/058,271
; EARLIER PILLING DATE: 1997-09-08
; EARLIER PILLING DATE: 1997-09-08
; MUMBER: OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO I
   LENGTH: 548
; TYPE: PRT
   TYPE: PRT
   GGRANISM: HUMAN
                                                                                                                                                                                                                                               Sequence 1, Application US/09139617
Patent No. 6222015
GENERAL INFORMATION:
                                                                                                                                                                                                                      RESULT 2
US-09-139-617-1
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RESULT US-09- US	561-741A-1 ence 1, Application US/09561741A ence 1, Application US/09561741A RAL INFORMATION: ULE OF INVENTION: ESTROGEN RECEPTOR E REPERENCE: 2004-79 RENT FILING DATE: 2000-04-26 OR APPLICATION NUMBER: 09/139,617 OR APPLICATION NUMBER: 09/139,617 OR APPLICATION NUMBER: 60/069,271 OR PILING DATE: 1997-09-08 OR FILING DATE: 1997-09-10 OR FILING DATE: 1997-09-10 ID NO 1 SMCTH: 548 NGCTH: 548 GANISM: HUMAN	
9 8 8	Ouery Match Best Local Similarity 100.0%; Pred. No. 1.5e-291; Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0	õ
& 4g	1 MDIKNSPSSLNSPSSYNCSQSILPLEHGSIYIPSSYVDSHHEYPAMTFYSFAVMYSIPS 60	
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è 8	241 CAGKAKRSGGHAPRVRELLLDALSBEQLVLTLLEAEBPHVLISRPSAPFTEASMMSLTK 300 [	<b>⊙</b> ∞
8 8	301 LADKELVHMISWAKKIPGFVELSLFDQVRLLESCWNEVLMWGLMWRSIDHPGKLIFAPDL 360 	0 0
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CAGKAKRSGGHAPRVRELLLDALSPEQLVLTLLEAEPPHVLISRPSAPFTEASMMMSLTK 300
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                                                                                                                                                                                                                                                                                                             Length 548;
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                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 2805; DB 4; Best Eocal Similarity 100.0%; Pred. No. 1.5e-291; Matches 530; Conservative 0; Mismatches 0;
                                    GENERAL INCOMENTATION, HILARY
TITLE OF INVENTION: ESTROGEN RECEPTOR
FILE REPERENCE: 20047V
CURRENT APPLICATION NUMBER: US/09/558,795
CURRENT FILING DATE: 2000-04-26
PRIOR PRIOR PRILING DATE: 1998-08-25
PRIOR FILING DATE: 1997-09-08
PRIOR FILING DATE: 1997-09-08
PRIOR FILING DATE: 1997-09-08
PRIOR FILING DATE: 1997-09-08
SEQ ID NO 1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Orphan receptor
NUMBER OF SEQUENCES: 19
COMPUTER READABLE FORM:
MEDIUM TYPE: ?loppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08836620A
Patent No. 5958710
Sequence 1, Application US/09558795
               Patent No. 6562592
GENERAL INFORMATION:
                                                                                                                                                                                                                                         LENGTH: 548
TYPE: PRT
ORGANISM: HUMAN
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US-09-558-795-1
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/836,620A

PRIOR APPLICATION DATA:
PRING DATE:
PRIOR APPLICATION DATA:
PRING DATE:
APPLICATION NUMBER: PCT/EP96/03933
FILING DATE:
APPLICATION NUMBER: GB 9518272.1
FILING DATE: GB-SEP-1995
PRIOR APPLICATION NUMBER: GB 9605550.4
FILING DATE: 15-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9607532.0
PRING APPLICATION NUMBER: GB 9607532.0
PRING APPLICATION NUMBER: GB 9609576.5
PRING APPLICATION NUMBER: GB 9609576.5
PRING APPLICATION NUMBER: GB 9609576.5

INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 485 amino acids

: 485 amino acids amino acid GY: linear

ORIGINAL SOURCE

TOPOLOGY:

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                                                                                                    1 HIFYSPAWMYSIPSNVTNLEGGPGRQTISPNVLWPTPGHLSPLVVHRQESHLYABPQKS
                                                                                      46 MTFYSDAVMYSIPSNVTNLEGGPGROTISPNVLWPTPGHLSPLVVHRQLSHLYAEPQKS
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                                                              Gaps
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o
                                    Length 485
                                                            1; Indels
                                   91.1%; Score 2554; DB 2;
99.8%; Pred. No. 9.7e-265;
iive 0; Mismatches 1;
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US-09-608-088-5
; Sequence 5, Application US/09608088
ORGANISM: Homo sapiens
                                      Query Match
Best Local Similarity 99.8
Matches 484; Conservative
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ilarity 100.0%; Pred. No. 2.5e-261;
Conservative 0; Mismatches 0; Indels
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Patent No. 5958710
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Orphan receptor
NUMBER OF SEQUENCES: 19
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DGS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPC)
CURRENT APPLICATION DATA:
GENERAL INCORRANTION:
APPLICANT: Mosselman, Sietse
APPLICANT: Mosselman, Sietse
APPLICANT: Mosselman, Sietse
APPLICANT: Dijkema, Rein
TITIE OF INVENTION: No. 6680368el Estrogen Receptor
TITIE OF INVENTION: No. 6680368el Estrogen Receptor
FILE REFERENCE: 0/96193 US/DI;
CURRENT APPLICATION NUMBER: US/09/608,088
CURRENT FILING DATE: 1997-03-26
PRIOR APPLICATION NUMBER: EP 96203284.3
PRIOR PILING DATE: 1996-11-22
PRIOR FILING DATE: 1996-11-22
PRIOR FILING DATE: 1996-03-26
NUMBER: OF SEQ ID NOS: 28
SOFTWARE: Patentin Version 3.0
SEQ ID NO 5.
                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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477; Conserv
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US-08-836-620A-2
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US-09-608-088-5
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Best Local S
Matches 477
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FILING DATE:
PALOR APPLICATION DATA:
APPLICATION NUMBER: PCT/BP96/03933
FILING DATE: 08-SEP-1995
PILING DATE: 08-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9605550.4
FILING DATE: 15-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 485 anino acids

Rattus rattus

ORIGINAL SOURCE: ORGANISM: Rat TOPOLOGY:

US-08-836-620A-2

amino acid GY: linear

US/08/836,620A

APPLICATION NUMBER:

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                                                                                                                                       61 PWCEARSLEHTLPVNRETLKRKLSGSSCASPVTSPNAKRDAHFCPVCSDYASGYHYGVWS
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                                                                             1 MTFYSPAVMNYSVPGSTSNLDGGPVRLSTSPNVLMPTSGHLSPLATHCQSSLLYAEPQKS
                                                                                                                        106 PWCBARSLEHTLPVNRETLKRKVSGNRCASPVTGPGSKRDAHFCAVCSDYASGYHYGVWS
                                                                                                                                                                                    166 CEGCKAPFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLRKCYEVGWVKCGSRRERCG
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                               Gaps
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0
 Length 485;
                             Indels
Query Match 81.7%; Score 2291; DB 2;
Best Local Similarity 88.7%; Pred. No. 1.5e-236;
Matches 430; Conservative 23; Mismatches 32;
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Sequence 13, Application US/08836620A

Setent No. 5958710

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION:
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RESULT 9
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 NUMBER OF SEQUENCES: 19
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,620A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81.5%; Score 2286; DB 2;
88.6%; Pred. No. 5.3e-236;
tive 23; Mismatches 32;
                                                                                                                                                                         APPLICATION WUMBER: GB 9518272.1
PILING DATE: 08-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9605550.4
FILING DATE: 15-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAX-1996
FILING DATE: 08-MAX-1996
FILING DATE: 08-MAX-1996
SEQUENCE CHARACTERISTICS:
                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/BP96/03933
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 484 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
ORGANISM: Rattus rattus
US-08-836-620A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 88.61
Matches 429; Conservative
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301 RSIDHPGKLIPAPDLVLDRDBGKCVEGILEIFDMLLATTARFRELKLQHKEYLCVKAMIL 360
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                                                                                                                                                                                             #1.25
                                                                                                                                                                                             do
                                                     APPLICANT:
TITLE OF INVENTION: Orphan receptor
TITLE OF INVENTION: Orphan receptor
NUMBER OF SEQUENCES: 19
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/03933
FILING DATE: BPLICATION NUMBER: GB 9518272.1
APPLICATION NUMBER: GB 9518272.1
PRIOR APPLICATION DATE: BPLICATION DATE: APPLICATION NUMBER: GB 9605550.4
FILING DATE: 15-MAR-1996
PRIOR APPLICATION DATA: APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
PRIOR APPLICATION DATA: APPLICATION NUMBER: GB 9609576.5
FILING DATE: GB-MAY-1996
INPORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
BENDURAL 485 amino acids
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Sequence 5, Application US/08836620A; Patent No. 5958710; GENERAL INFORMATION:
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ORGANISM: Mus musculus
US-08-836-620A-5
                                                                                                                                                                                                            CURRENT APPLICATION DATA APPLICATION NUMBER: US PILING DATE:
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TOPOLOGY: linear
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ORGANISM: Homo sapiens
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Matches 415; Conserv
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TYPE: PRT
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US-09-608-088-6
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421 RHISNKGMEHLLSMKCKNVVPVYDLLLEMLNAHTLRGYKSSISGSGCCSTEDSKSKEGSQ 480
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80.6%; Score 2262; DB 2; Length 484;
Best Local Similarity 88.0%; Pred. No. 2e-233;
Matches 426; Conservative 23; Mismatches 35; Indels (
                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,620A
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: GB 9518272.1
PILING DATE: 08-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 960550.4
PILING DATE: 15-WAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-PR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9609576.5
PILING DATE: 08-WAY-1996
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE GRAZACTEREISTICS:
LENGTH: 444 Amino acids
                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/03933
                                                                                                                                                                                                             APPLICANT:
TITLE OF INVENTION: Orphan receptor
NUMBER OF SEQUENCES: 19
COMPUTER READABLE FORM:
MEDIUM TYBE: PLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                    Orphan receptor
                                                                                                                                    US-08-836-620A-14
; Sequence 14, Application US/08836620A
; Parent No. 5958710
; GENERAL INFORMATION:
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amino acid
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                                   526 NPQSQ 530
                                                                    481 NLOSO 485
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466 RFASNKGMEHLLAWKCKNVVPVYDLLLEMLNAHVLRGCKSSITGSBCSPAEDSKSKBGSQ 525
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                                              114 EHTLEVNRETLKRKVSGNRCASPYTGPGSRRDAHFCAVCSDYASGYHYGVWSCEGCKAFF 173
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LINSSMYPEVTATODADSSRKLAHELLNAVTDALVWVIAKSGISSOOOSMRLANLLMLLSHV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 669368
| Patent No. 669368
| GENERAL INPORMATION:
| APPLICANT: Mosselman, Sietse APPLICANT: Dijkema, Rein | TITLE OF INVENTION: No. 66803681 Estrogen Receptor: FILE REFERENCE: O/96193 US/D1 | CURRENT APPLICATION NUMBER: US/09/608,088 | CURRENT FILING DATE: 2000-06-30 | PRIOR FILING DATE: 1997-03-26 | PRIOR FILING DATE: 1996-11-22 | PRIOR FILING DATE: 1996-11-22 | PRIOR FILING DATE: 1996-11-22 | PRIOR FILING DATE: 1996-03-26 | PRIOR PRIOR PRIOR FILING DATE: 1996-03-26 | PRIOR FILING DATE: 1996-0
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LRKCYEVGMVKCGSRRERCGYRLVRRQRSADEQLHCAGKAKRSGGHAPRVRELLLDALSP 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 AHPCAVCSDYASGYHYGVWSCEGCKAPFKRSIQGHNDYICPATNQCTIDIQNRRKSCQACR 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 EQLVLTLLEAEPPHVLISRPSAPFTEASMMSLTKLADKELVHMISWAKKIPGFVELSLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146 AHFCAVCSDYASGYHYGVWSCEGCKAFFRRSIQGHNDYICPATNQCTIDKNRRKSCQACR
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Sequence 12, Application US/08764870

Sequence 12, Application US/08764870

Sequence 12, Application US/08764870

APPLICANT: Scanlan, Thomas S

APPLICANT: Baxter, John D

APPLICANT: Fleterick, Robert J

APPLICANT: Fleterick, Robert J

APPLICANT: Wagner, Richard L

APPLICANT: West, Brian

APPLICANT: West, Brian

APPLICANT: West, Brian

TITLE OF INVENTION: Binding Domains

TITLE OF INVENTION: Binding Domains

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooley Godward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 71.9%; Score 2017; DB 2; Length 384; Best Local Similarity 100.0%; Pred. No. 2.5e-207; Matches 383; Conservative 0; Mismatches 0; Indels (
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP96/03933
FILING DATE:
APPLICATION NUMBER: GB 9518272.1
FILING DATE:
PRIOR APPLICATION NUMBER: GB 9518272.1
FILING DATE:
APPLICATION NUMBER: GB 960550.4
FILING DATE: 15-MAR.1996
FILING DATE: 15-MAR.1996
FILING DATE: 11-MAR.1996
FILING DATE: 11-APR.1996
FILING DATE: 11-APR.1996
FILING DATE: 11-APR.1996
FILING DATE: 11-APR.1996
FILING DATE: GB 9609576.5
FILING DATE: GB-MAY.1996
FILING DATE: GB-M
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ORGANISM: Homo sapiens
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US-08-356-620A-15
US-08-356-620A-15
Sequence 15, Application US/08836620A
Fatent No. 5958710
CENERAL INFORMATION:
TITLE OF INVENTION: Orphan receptor
NUMBER OF SEQUENCES: 19
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/836,620A
FILING DATE:
                                 Sequence 21, Application US/09608088
| Patent No. 6680368
| GRNERAL INFORMATION:
| APPLICANT: Mosselman, Sietse | APPLICANT: Mosselman, Sietse | APPLICANT: Mosselman, Sietse | APPLICANT: Dijkema, Rein | TITLE OF INVENTION: No. 6680368el Estrogen Receptor | TITLE OF INVENTION: No. 6680368el Estrogen Receptor | FILE REFERENCE: 0/96193 US/D1 | CURRENT PTLING DATE: 2000-06-30 | PRIOR FILING DATE: 1997-03-26 | PRIOR FILING DATE: 1997-03-26 | PRIOR PILING DATE: 1996-11-22 | PRIOR PILING DATE: 1996-03-26 | NUMBER OF SEQ ID NOS: 28 | SOFTWARE: Patentin version 3.0 | SEQ ID NO 21 | LENGTH: 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
US-09-608-088-21
                       US-09-608-088-21
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WESULT 15
US-08-980-115-12
US-08-980-115-12
Sequence 12, Application US/08980115
Patent No. 6266622
GENERAL INFORMATION;
APPLICANT: Scanlan, Thomas S.
APPLICANT: Baxer, John D.
APPLICANT: Baxer, John D.
APPLICANT: Feterick, Robert J.
APPLICANT: Magner, Peter J.
APPLICANT: Magner, Richard L.
APPLICANT: Magner, Nachard L.
APPLICANT: Magner, Nachard L.
APPLICANT: Magner, Nachard L.
APPLICANT: Magner, Nachard N.
APPLICANT: Magner, Nachard N.
APPLICANT: Magner, 1040-246/0205
CURRENT Shiau, Andrew K.
TITLE OF INVENTION NUMBER: US/08/980,115
CURRENT FILING DATE: 1997-11-26
EARLIER APLICATION NUMBER: 60/008,506
EARLIER APLICATION NUMBER: 60/008,506
EARLIER PILING DATE: 1995-12-13
EARLIER PILING DATE: 1995-12-13
MUMBER: PAPLICATION NUMBER: 60/008,540
EARLIER PILING DATE: 1995-12-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :| | | ::| | | ::: :| | : : | | :| | 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 POKSPWC--EARSLEHTLPVNRETLKRKVSGNRCASPVTGPG----SKRDAHFCAVCSD 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 NELEPLARP-----QLKIPLERPLGEVYLDSSKPAVYNYPEGAAYERVAAAAAAAAAAA 74
                                                                                                                     155 YASGYHYGVWSCEGCKAPPKRSIQGHNDYICPATNQCTIDKNRRKSCQACRIRKCYEVGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 NSPSSLNSPSSYNCSQSILPLEH--GSIYIPSS--YVDSHHEYPAMTFYSPAVMNYSIPS
                                                                          436 ALVWVIAKSGISSOCOSMRLANLIMLISHVRHASNKGMEHLINMKCKNVVPVYDLILLEML
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44.0%; Score 1233.5; DB 3; Length 595;
Best Local Similarity 48.4%; Pred. No. 5.2e-123;
Matches 264; Conservative 88; Mismatches 128; Indels 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215 VKCGSRRERCGYRLVRRQRSADBQLHCAGKAKRSGGHAPRVR-----
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NAME/KEY: DOWAIN

COCATION: (287)...(549)

COTHER INFORMATION: minimal ligand binding domain
15-08-980-115-12
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                                                                                                                                                                                                                                                                                496 NAHVL 500
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                                                  259 LEDALSPEQLVITELEAEPPHVLISR--PSAPPTEASMYMSLTKLADKELVFMISWAKKI 316 | :|::|::|| ||:|||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| 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44.0%; Score 1233.5; DB 3; Length
Best Local Similarity 48.4%; Pred, No. 5.2e-123;
Matches 264; Conservative 88; Mismatches 128; Indels
STREET: Five Palo Alto Square, 3000 El Camillo Real STATE: CA COUNTRY: DEAL CALLO STATE: CA COUNTRY: USA ZIP: 94306

ZIP: 94306

COMPUTER READALE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentl Release #1.0, Version #1.30 SOFTWARE: Patentl Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/764,870 FILING DATE: 13-DEC-1996 CLASSIFICATION NUMBER: US 60/008,540 FILING DATE: 13-DEC-1995 PRIOR APPLICATION NUMBER: US 60/008,543 FILING DATE: 13-DEC-1995 PRIOR APPLICATION NUMBER: US 60/008,606 FILING DATE: 14-DEC-1995 ATOMNEY/AGENT INPORMATION: APPLICATION NUMBER: US 60/008,606 FILING DATE: 14-DEC-1995 ATOMNEY/AGENT INPORMATION: NAME: US 60/008,606 FILING DATE: 14-DEC-1995 ATOMNEY/AGENT INPORMATION: NAME: USCALE NUMBER: USAL-246/01US TELEPHONE: (650)843-5000 INPORMATION INPORMATION: TELEPHONE: (650)843-5000 INPORMATION INPORMATION: SEQUENCE CHERENTS/INS: LENGTH: 595 amino acids TRANDENES: MOORTH AND ACID ATOMNEY INDEAR.
                                          El Camino Real
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MOLECULE TYPE: protein
US-08-764-870-12
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Search completed: June 20, 2004, 10:39:47 Job time : 25 secs